

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:17 ; Search time 17695.9 Seconds  
(without alignments)  
16.701 Million cell updates/sec

Title: US-09-757-100B-17

Perfect score: 20

Sequence: 1 attctcgtcgtggtggaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/US08\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*

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55: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq:\*

56: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq:\*

57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq:\*

58: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq:\*

59: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq:\*

60: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	1	PCT-US00-18999-17
2	20	100.0	20	17	US-09-377-310-17
3	20	100.0	20	29	US-09-757-100B-17
c 4	15.2	76.0	4	8	US-08-466-588-52
5	15	75.0	15	1	PCT-US00-18999-37
6	15	75.0	15	17	US-09-377-310-37
7	15	75.0	15	29	US-09-757-100B-37
8	14.8	74.0	35	15	US-09-144-428-31
9	14.8	74.0	35	16	US-09-241-913B-31
10	14.8	74.0	35	18	US-09-441-966-31
11	14.4	72.0	37	8	US-08-472-801-1314
12	14.4	72.0	37	10	US-08-668-235-1314
13	14.2	71.0	20	1	PCT-US97-06104-16
14	13.6	68.0	25	55	US-60-232-638-132115
15	13.6	68.0	25	55	US-60-234-017-326383
c 16	13.4	67.0	18	14	US-09-082-614-16
c 17	13.2	66.0	19	53	US-60-216-745-5602
c 18	13.2	66.0	20	13	US-08-965-620-718
c 19	13.2	66.0	25	26	US-09-660-220-136892
c 20	13.2	66.0	25	55	US-60-233-166-57027
c 21	13.2	66.0	25	55	US-60-233-166-384424
c 22	13.2	66.0	43	17	US-09-310-298-3092
c 23	13	65.0	25	55	US-60-233-166-260192
c 24	12.8	64.0	19	27	US-09-696-791-539
25	12.8	64.0	20	28	US-09-703-708-11309
26	12.8	64.0	20	28	US-09-703-708-17076
27	12.8	64.0	20	48	US-60-164-320-11309
28	12.8	64.0	20	48	US-60-164-320-17076
29	12.8	64.0	20	50	US-60-183-791-11309
30	12.8	64.0	20	50	US-60-183-791-17076
31	12.8	64.0	21	1	PCT-US97-07972-3
32	12.8	64.0	21	10	US-08-647-351A-3
33	12.8	64.0	21	15	US-09-100-649A-3
34	12.8	64.0	21	17	US-09-326-074-3
35	12.8	64.0	25	55	US-60-233-166-221240
c 36	12.8	64.0	25	55	US-60-234-017-9806
c 37	12.8	64.0	25	55	US-60-234-017-9815
c 38	12.8	64.0	25	55	US-60-234-017-336454
c 39	12.8	64.0	25	55	US-60-234-017-336457
c 40	12.8	64.0	25	55	US-60-234-017-336458
c 41	12.8	64.0	31	18	US-09-465-684-134
c 42	12.8	64.0	40	18	US-09-404-520-30598
c 43	12.6	63.0	20	1	PCT-US00-00583-43
c 44	12.6	63.0	25	55	US-60-233-166-70907
c 45	12.6	63.0	25	55	US-60-234-017-229508

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-17  
; Sequence 17, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-17

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20  
Db 1 attctcgtcgtggtgaa 20  
|||||

RESULT 2  
US-09-377-310-17  
; Sequence 17, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-17

Query Match 100.0%; Score 20; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20  
Db 1 attctcgtcgtggtgaa 20  
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RESULT 3  
US-09-757-100B-17  
; Sequence 17, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-17

Query Match 100.0%; Score 20; DB 29; Length 20;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20  
Db 1 attctcgtcgtggtgaa 20  
|||||

RESULT 4  
US-08-466-588-52/c  
; Sequence 52, Application US/08466588  
; GENERAL INFORMATION:  
; APPLICANT: Sukhatme, Vikas P.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 North Clark Street, Suite 800  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/466,588  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/040,548  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coughlin, Daniel F.  
; REGISTRATION NUMBER: 36,111  
; REFERENCE/DOCKET NUMBER: arcd067  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 744-0090  
; TELEFAX: (312) 245-4961  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:40 ; Search time 876.95 seconds  
(without alignments)  
14.320 Million cell updates/sec

Title: US-09-757-100B-12

Perfect score: 20

Sequence: 1 cctgacatcagtagcatctc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	22 AAC65544	Human focal adhesi
c 2	16.4	82.0	20	21 AAC58860	Human tumour suppr
3	15	75.0	15	22 AAC65564	Human focal adhesi
c 4	14.2	71.0	21	22 AAF95492	Human gene single
c 5	13.6	68.0	39	21 AAA51849	Primer mcl-like-2f
6	13.6	68.0	40	21 AAA51848	Primer mcl-like-1r
c 7	13.6	68.0	42	13 AAO23448	Human heavy chain
c 8	13.6	68.0	42	14 AAO44160	Probe to isolate h
c 9	13.6	68.0	42	14 AAO44180	Probe specific for
c 10	13.6	68.0	42	17 AAT37238	Human antibody hea
c 11	13.6	68.0	42	17 AAT37216	Human antibody J s

c 12	13.6	68.0	42	18 AAV12514	Probe for human J
c 13	13.6	68.0	42	18 AAT70497	Human Immunoglobul
c 14	13.6	68.0	42	18 AAT73468	Human heavy chain
c 15	13.6	68.0	42	18 AAT73448	Human J-mu region
c 16	13.6	68.0	42	19 AAV38155	Probe oligo-1 for
c 17	13.6	68.0	42	19 AAV38128	Probe used to isol
c 18	13.6	68.0	42	20 AAZ21891	Probe used to isol
c 19	13.6	68.0	42	20 AAZ22071	Probe used to isol
c 20	13.6	68.0	42	20 AAX06008	US5874299 Seq ID 1
c 21	13.2	66.0	30	18 AAT58419	Apollipoprotein A g
c 22	13.2	66.0	30	20 AAV82530	Probe Aposma-1 use
c 23	13	65.0	23	19 AAV50010	Oligonucleotide SE
c 24	13	65.0	23	20 AAX18226	Primer lRAF616 for
c 25	13	65.0	23	21 AAX88383	FAR1 gene amplific
c 26	13	65.0	36	17 AAX65443	Mouse B7-1 hammerh
c 27	12.8	64.0	21	17 AAT39326	Primer EL074 to ge
c 28	12.8	64.0	21	17 AAT35891	Newcastle disease
c 29	12.8	64.0	21	17 AAT35924	Newcastle disease
c 30	12.8	64.0	21	19 AAV07013	Primer EL074 for N
c 31	12.8	64.0	21	19 AAV42526	PCR primer EL074 u
c 32	12.8	64.0	27	16 AAO76135	Human MDC PCR prim
c 33	12.8	64.0	28	22 AAA99419	PCR primer SEQ ID
c 34	12.6	63.0	27	18 AAX63148	Delta-9 desaturase
c 35	12.6	63.0	29	21 AAZ87393	Human thrombopoiet
c 36	12.4	62.0	27	18 AAX68545	Hammerhead ribozym
c 37	12.4	62.0	29	21 AAF00661	Human fit1 VEGF re
c 38	12.4	62.0	38	16 AAT53885	Rat ICAM hammerhea
c 39	12.4	62.0	50	17 AAT40112	Human Mer receptor
c 40	12.2	61.0	20	21 AAA78278	Human Ig H chain s
c 41	12.2	61.0	20	21 AAA78291	Human Ig H chain s
c 42	12.2	61.0	25	16 AAO94416	Rat farnesyl prote
c 43	12.2	61.0	27	13 AAO30098	JH probe #3 to det
c 44	12.2	61.0	28	20 AAX88103	Antifreeze protein
c 45	12.2	61.0	29	20 AAX88102	Synthetic antifree

ALIGNMENTS

RESULT 1

AAC65544  
ID AAC65544 standard; DNA; 20 BP.

XX

AC AAC65544;

XX

DT 12-FEB-2001 (first entry)

XX

DE Human focal adhesion kinase antisense sequence #10.

XX

KW Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX

OS Homo sapiens.

XX

PN US6133031-A.

XX

PD 17-OCT-2000.

XX

PF 19-AUG-1999; 99US-0377310.

XX

PR 19-AUG-1999; 99US-0377310.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Gaarde WA;

XX

DR WPI; 2001-006141/01.

XX

PT New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX

```
PS Claim 15; Column 23; 30pp; English.
XX
CC The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.
XX
SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 other;

Query Match      100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   |||||
DB 1 cctgacatcagtagcatctc 20

RESULT 2
AAC58860/c
ID AAC58860 standard; DNA; 20 BP.
AC AAC58860;
XX
XX
XX 25-JAN-2001 (first entry)
XX
XX Human tumour suppressor BRG1 deletion analysis PCR primer BRG1.R1.
XX
XX Human; BRG1; tumour suppressor gene; cancer; chromosome 19p13.1;
XX retinoblastoma tumour suppressor gene; RB; drug screening; gene therapy;
XX drug design; peptide therapy; animal model; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200056931-A1.
XX
XX 28-SEP-2000.
XX
XX 23-MAR-2000; 2000WO-US07678.
XX
XX 23-MAR-1999; 99US-0125806.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Wong AKC, Tavtigian SV, Teng DH;
XX
XX WPI; 2000-587668/55.
XX
XX Diagnosing a polymorphism associated with predisposition for cancer in
XX humans by determining whether there is a germline alteration of a BRG1
XX gene or its expression products -
XX
XX Example 2; Page 51; 215pp; English.
XX
XX The present invention is concerned with the use of the human tumour
XX suppressor gene BRG1 in cancer diagnosis and therapy. This gene is
XX comprised of several exons, shown in AAC58874-C58903, and has several
XX splice variants, given in AAC58906-C58912. The protein sequences for
XX these are shown in AAB27552-B27558. BRG1 is a homologue of the Drosophila
XX protein brahma, and has been shown to be bound to retinoblastoma tumour
XX suppressor protein RB. The BRG1 coding sequence and protein can be used
XX in the diagnosis and treatment of cancer (for example by gene therapy);
XX particularly prostate cancer, to identify drugs useful in the treatment
XX of cancer and in the production of animal models for cancer. Sequences
XX AAC58849-C58873 are all primers used in the isolation and sequencing of
XX the BRG1 gene and its variants.
XX
XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;

Query Match      82.0%; Score 16.4; DB 21; Length 20;
Best Local Similarity 94.4%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgacatcagtagcatct 19
   ||| |||||
DB 20 CTGGCATCAGTAGCATCT 3

RESULT 3
AAC65564
ID AAC65564 standard; DNA; 15 BP.
XX
XX AAC65564;
XX
XX 12-FEB-2001 (first entry)
XX
XX Human focal adhesion kinase antisense sequence #30.
XX
XX Human; focal adhesion kinase; FAK; signal transduction; cancer;
XX embryonic development disorder; angiogenic disorder; wound healing;
XX antisense; phosphorothioate; ss.
XX
XX Homo sapiens.
XX
XX US6133031-A.
XX
XX 17-OCT-2000.
XX
XX 19-AUG-1999; 99US-0377310.
XX
XX 19-AUG-1999; 99US-0377310.
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Gaarde WA;
XX
XX WPI; 2001-006141/01.
XX
XX New antisense compounds for inhibiting focal adhesion kinase
XX expression, especially useful for inhibiting retinal
XX neovascularization, or for diagnosing and treating e.g. colon cancer -
XX
XX Example 2; Column 25; 30pp; English.
XX
XX The present invention describes a number of phosphorothioate antisense
XX sequences to the human focal adhesion kinase (FAK) protein. This protein
XX is involved in integrin-mediated signal transduction, and is implicated
XX in cancer, particularly colon, breast and oral tumours, embryonic
XX development disorders, angiogenic disorders and wound healing. The
XX antisense sequences, including the one shown here, can be used in the
XX treatment of all of these.
XX
XX Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 other;

Query Match      75.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgacatcagtagcat 17
   |||||
DB 1 tgacatcagtagcat 15

RESULT 4
AAF95492/c
ID AAF95492 standard; DNA; 21 BP.
XX
XX AAF95492;
XX
XX 06-JUN-2001 (first entry)
XX
XX
```



XX DE Human gene single nucleotide polymorphism #253.

XX KW Human: variant thrombospondin 1; variant thrombospondin 4; SNP;

XX KW polymorphism; vascular disease; coronary artery disease; forensics;

XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

XX KW pulmonary embolism; paternity test; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Variation replace(11,A)

XX FT /\*tag= a

XX FT /standard\_name= "single nucleotide polymorphism"

XX PN WO200118250-A2.

XX PD 15-MAR-2001.

XX PF 07-SEP-2000; 2000WO-US24503.

XX PR 10-SEP-1999; 99US-0153357.

XX PR 26-JUL-2000; 2000US-0220947.

XX PR 16-AUG-2000; 2000US-0225724.

XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;

XX DR WPI; 2001-226749/23.

XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in

XX PT applications such as forensics, paternity testing, medicine, genetic

XX PT analysis and phenotype correlations to diseases such as diabetes and

XX PT atherosclerosis -

XX PS Examples; Page 67; 242pp; English.

XX CC The present invention provides a method of diagnosing a vascular disease

XX CC in an individual, involving determining the sequence at various

XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4

XX CC genes. The sequences at a number of polymorphic sites are also provided

XX CC in the specification. In particular, the method can be used in the

XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart

XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism

XX CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

XX CC useful in forensics, paternity testing, genetic analysis and phenotype

XX CC correlations to diseases. The present sequence is an example of one of

XX CC the human gene SNPs shown in the specification.

XX SQ Sequence 21 BP; 7 A; 4 C; 7 G; 3 T; 0 other;

Query Match 71.0%; Score 14.2; DB 22; Length 21;

Best Local Similarity 84.2%; Pred. No. 2.9e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatct 19

DB 19 CTTGCCATCAGTGGCATCT 1

RESULT 5

AAA51849/c

ID AAA51849 standard; DNA; 39 BP.

XX AC AAA51849;

XX AC AAA51849;

XX DT 09-JAN-2001 (first entry)

XX DE Primer mcl-like-2f for human MC-R1 exon 2 amplification.

KW MC-R1; melanocortin 1 receptor; rhodopsin; G-protein coupled receptor;

KW splice variant; MC-R1B; C-terminal extension; agonist; antagonist;

KW modulator; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200039147-A1.

XX PD 06-JUL-2000.

XX PF 16-DEC-1999; 99WO-US29963.

XX PR 23-DEC-1998; 98US-0113401.

XX PA (MERI ) MERCK & CO INC.

XX PI Howard AD, MacNeil DJ, Van Der Ploeg LHT;

XX DR WPI; 2000-452365/39.

XX PT New nucleic acid encoding a human melanocortin 1 receptor protein

XX PT (MC-R1B) for determining whether a substance is capable of binding to

XX PT or activating human MC-R1B and identifying a substance that modulates

XX PT MC-R1B receptor activity

XX PS Example 1; Page 49; 101pp; English.

XX CC The invention concerns novel splice variants of the melanocortin 1

XX CC receptor (MC-R1) protein belonging to the rhodopsin sub-family of

XX CC G-protein coupled receptors. The splice variants, referred to as MC-R1B

XX CC proteins, contain an intracellular domain with an additional 65 amino

XX CC acid residues in comparison to previously disclosed human MC-R1, referred

XX CC to as MC-R1A. Additionally, residue 317 of the MC-R1B proteins is Cys,

XX CC whereas the C-terminal amino acid residue 317 of known MC-R1A proteins is

XX CC Trp. The novel sequences can be used to determine whether a substance is

XX CC modulates MC-R1B receptor activity and to identify potential agonists or

XX CC antagonists of MC-R1B. Pharmaceutical compositions comprising

XX CC modulators of MC-R1B are used to treat or diagnose disorders involving

XX CC inappropriate melanocortin expression or activity.

XX SQ Sequence 39 BP; 5 A; 16 C; 9 G; 9 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 39;

Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20

DB 22 CCTGAGAGCAGGAGCATGTC 3

RESULT 6

AAA51848

ID AAA51848 standard; DNA; 40 BP.

XX AC AAA51848;

XX AC AAA51848;

XX DT 09-JAN-2001 (first entry)

XX DE Primer mcl-like-1r for human MC-R1 exon 1 amplification.

XX KW MC-R1; melanocortin 1 receptor; rhodopsin; G-protein coupled receptor;

XX KW splice variant; MC-R1B; C-terminal extension; agonist; antagonist;

XX KW modulator; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200039147-A1.

XX PD 06-JUL-2000.

XX PF 16-DEC-1999; 99WO-US29963.

XX PR 23-DEC-1998; 98US-0113401.  
 XX PA (MERI ) MERCK & CO INC.  
 XX PI Howard AD, MacNeil DJ, Van Der Ploeg LHT;  
 XX WPI; 2000-452365/39.  
 XX  
 XX New nucleic acid encoding a human melanocortin 1 receptor protein  
 PT (MC-R1B) for determining whether a substance is capable of binding to  
 PT or activating human MC-R1B and identifying a substance that modulates  
 PT MC-R1B receptor activity  
 XX  
 XX Example 1; Page 49; 101pp; English.  
 XX  
 XX The invention concerns novel splice variants of the melanocortin 1  
 CC receptor (MC-R1) protein belonging to the rhodopsin sub-family of  
 CC G-protein coupled receptors. The splice variants, referred to as MC-R1B  
 CC proteins, contain an intracellular domain with an additional 65 amino  
 CC acid residues in comparison to previously disclosed human MC-R1, referred  
 CC to as MC-R1A. Additionally, residue 317 of the MC-R1B proteins is Cys,  
 CC whereas the C-terminal amino acid residue 317 of known MC-R1A proteins is  
 CC Trp. The novel sequences can be used to determine whether a substance  
 CC modulates MC-R1B receptor activity and to identify potential agonists or  
 CC antagonists of MC-R1B. Pharmaceutical compositions comprising  
 CC modulators of MC-R1B are used to treat or diagnose disorders involving  
 CC inappropriate melanocortin expression or activity.  
 XX  
 XX Sequence 40 BP; 8 A; 12 C; 13 G; 7 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 40;  
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
 ||||| ||| ||||| ||  
 Db 9 cctgagagcaggagcatgtc 28

RESULT 7  
 AAQ23448/c  
 ID AAQ23448 standard; DNA; 42 BP.  
 AC AAQ23448;  
 XX  
 XX 17-AUG-1992 (first entry)  
 DT  
 XX Human heavy chain J region specific oligonucleotide.  
 DE Placental; probe; heavy chain; ss.  
 KW  
 KW Synthetic.  
 OS  
 XX WO9203918-A.  
 PN  
 XX 19-MAR-1992.  
 PD  
 XX 28-AUG-1991; 91WO-US06185.  
 PF  
 XX 31-AUG-1990; 90US-0575962.  
 PR  
 PR 29-AUG-1990; 90US-0574748.  
 XX  
 XX (GENP-) GENPHARM INT INC.  
 PA  
 XX Lonberg N, Kay R;  
 PI  
 XX WPI; 1992-113962/14.  
 DR  
 XX Immunoglobulin trans:genes - for prodn. of heterologous  
 PT non-rearranged and/or rearranged Ig chains  
 XX

PS Example 14; Page 82; 172pp; English.

XX A human placental genomic DNA library cloned into the phage vector  
 CC lambda EMBL3/SP6/T7 was screened with the human heavy chain J region  
 CC specific oligonucleotide probe and the phage clone lambda 1.3 isolated.  
 CC A 6 kb HindIII/KpnI fragment from this clone, contg. all six J segments  
 CC as well as D segment BHQ52 and the heavy chain J-mu intronic enhancer  
 CC was isolated, and ultimately used to construct an IgM expressing  
 CC mini-locus transgene.  
 CC See also Q23419-50, Q22417-30.

XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 13; Length 42;  
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
 || ||||| ||||| ||  
 Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 8  
 AAQ44160/c  
 ID AAQ44160 standard; DNA; 42 BP.

XX AAQ44160;  
 AC

DT 10-NOV-1993 (first entry)

XX Probe to isolate human immunoglobulin Joining segments.  
 DE Immunoglobulin; Ig; heavy chain; minilocus; isotype switching;  
 KW J region; ss.  
 KW  
 XX Synthetic.

XX WO9312227-A.

XX 24-JUN-1993.

XX 17-DEC-1992; 92WO-US10983.  
 PF  
 XX 17-DEC-1991; 91US-0810279.  
 PR  
 PR 18-MAR-1992; 92US-0853408.  
 PR  
 PR 23-JUN-1992; 92US-0904068.

XX (GENP-) GENPHARM INT INC.

XX Kay RM, Lonberg N;

XX WPI; 1993-214169/26.

XX Transgenic non-human animals contg. immunoglobulin heavy chain  
 PT trans gene - used to produce useful antibodies by isotype  
 PT switching  
 PT  
 XX Example 4; Page 60; 196pp; English.

XX A 6.3kb BamHI/HindIII fragment that includes all J segments was  
 CC isolated from human genomic DNA library using probe AAQ44160. An  
 CC adjacent 10kb HindIII/BamHI fragment that contains enhancer, switch  
 CC and constant region coding exons was similarly isolated using the  
 CC probe AAQ44161 and an adjacent 3' 1.5kb BamHI fragment was isolated  
 CC using pMUM insert as probe and cloned into pUC19. (pMUM is a 4kb  
 CC EcoRI/HindIII fragment isolated from human genomic DNA library with  
 CC oligonucleotide AAQ44162 mu membrane exon 1). All three fragments are  
 CC used in the construction of plasmid pHIG1 which contains an 18kb  
 CC insert encoding J and C-mu segments.

XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

```

Query Match      68.0%; Score 13.6; DB 14; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 9
AAQ44180/c
ID AAQ44180 standard; DNA; 42 BP.
XX
AC AAQ44180;
XX
DT 10-NOV-1993 (first entry)
XX
DE Probe specific for human heavy chain J region.
XX
KW Immunoglobulin; IgM; heavy chain; minilocus transgene;
KW isotype switching; J-mu constant region; Joining region; ss.
XX
OS Synthetic.
XX
PN W09312227-A.
XX
PD 24-JUN-1993.
XX
PF 17-DEC-1992; 92WO-US10983.
XX
PR 17-DEC-1991; 91US-0810279.
PR 18-MAR-1992; 92US-0853408.
PR 23-JUN-1992; 92US-0904068.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
WPI; 1993-214169/26.
XX
Transgenic non-human animals contg. immunoglobulin heavy chain
PT trans gene - used to produce useful antibodies by isotype
PT switching
XX
PS Example 12; Page 91; 196pp; English.
XX
CC A human placental genomic DNA library cloned into the phage vector
CC lambda EMBL3/SP6/T7 was screened with the human heavy chain
CC J-region specific oligonucleotide Q44180. Phage clone lambda 1.3 was
CC isolated. A 6kb HindIII/KpnI fragment from this clone, containing
CC all 6 J segments as well as D segment DHQ52 and the heavy chain
CC J-mu intronic enhancer, was isolated. The same library was screened
CC with the human mu specific oligonucleotide Q44181 and phage clone
CC lambda 2.1 isolated. A 10.5kb HindIII/XhoI fragment, containing the
CC mu switch region and all of the mu constant region exons, was
CC isolated from this clone. The two fragments were ligated together
CC with KpnI/XhoI digested pNN03 to obtain plasmid pJMI which was used
CC in the construction of IgM expressing minilocus transgene pIGM1.
XX
SQ Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match      68.0%; Score 13.6; DB 14; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 10

```

```

AAT37238/C
ID AAT37238 standard; DNA; 42 BP.
XX
AC AAT37238;
XX
DT 18-APR-1997 (first entry)
XX
DE Human antibody heavy chain J region specific probe.
XX
KW Heavy chain; J region; human; probe; minilocus; transgene;
KW transgenic; mouse; production; heterologous; antibody; IgM;
KW immunoglobulin; ss.
XX
OS Synthetic.
XX
PN US5545806-A.
XX
PD 13-AUG-1996.
XX
PF 29-AUG-1990; 90US-0574748.
XX
PR 16-DEC-1992; 92US-0990860.
PR 29-AUG-1990; 90US-0574748.
PR 31-AUG-1990; 90US-0575962.
PR 17-DEC-1991; 91US-0810279.
PR 18-MAR-1992; 92US-0853408.
PR 23-JUN-1992; 92US-0904068.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
WPI; 1996-383736/38.
XX
Prod. of heterologous human immunoglobulin(s) - by immunising
PT transgenic mice
XX
PS Example 12; Columns 57-58; 94pp; English.
XX
CC The present sequence is a probe specific for a human antibody heavy
CC chain J region, which was used in the construction of a IgM heavy
CC chain minilocus transgene. The transgene was injected into mouse
CC embryo pronuclei to generate transgenic mice, which can be used for
CC the production of heterologous (i.e. human) antibodies against
CC specific antigens, this comprises immunising a mouse with a
CC preselected antigen and collecting antigen binding heterologous
CC human IgM immunoglobulins.
XX
SQ Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match      68.0%; Score 13.6; DB 17; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 11
AAT37216/C
ID AAT37216 standard; DNA; 42 BP.
XX
AC AAT37216;
XX
DT 18-APR-1997 (first entry)
XX
DE Human antibody J segment oligonucleotide probe.
XX
KW Heavy chain; gene segment; human; DNA fragment; probe;
KW minilocus; transgene; transgenic; mouse; J segment;
KW production; heterologous; antibody; gamma; immunoglobulin; ss.

```



```

XX Synthetic.
OS Homo sapiens.
XX
XX US5633425-A.
XX
XX 27-MAY-1997.
XX
XX 05-FEB-1992; 92US-0834539.
XX
XX 29-AUG-1990; 90US-0574448.
XX
XX 31-AUG-1990; 90US-0575962.
XX
XX (GENP-) GENPHARM INT INC.
XX
XX Kay RM, Lonberg N;
XX
XX WPI; 1997-297410/27.
XX
XX Transgenic mouse for heterologous antibody production - containing
XX DNA encoding human immunoglobulin components
XX
XX Example 5; Column 33; 90pp; English.
XX
XX This oligonucleotide was used as a probe to facilitate in the
XX cloning of a J-mu region from a human immunoglobulin. The probe
XX isolated a 6.3 kb BamHI/HindIII fragment from a human genomic library
XX which included all joining (J) segments. This region is used in a novel
XX method of developing transgenic non-human animals capable of producing
XX heterologous antibodies encoded by human immunoglobulin genes. Such
XX transgenically produced monoclonal antibodies should alleviate the
XX intrinsic immunogenicity of non-human immunoglobulins allowing the
XX development of new in vivo applications.
XX
XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| |||||
DB 35 CCAGACATCAAAAGCATCAC 16

RESULT 14
AAT73468/C
ID AAT73468 standard; DNA; 42 BP.
XX
XX AAT73468;
XX
XX 23-JAN-1998 (first entry)
XX
XX Human heavy chain J region specific probe.
XX
XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
XX transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
XX transplant rejection; immunoglobulin; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9713852-A1.
XX
XX 17-APR-1997.
XX
XX 10-OCT-1996; 96WO-US16433.
XX
XX 10-OCT-1995; 95US-0544404.
XX
XX (GENP-) GENPHARM INT INC.
XX
XX Kay RM, Lonberg N;
XX
XX WPI; 1997-235888/21.
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
XX treatment of auto-immune disease etc.
XX
XX Example 4; Page 103; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply
XX present sequence represents a probe used to screen a human placental
XX genomic DNA library cloned into the phage vector lambdaEMBL3/SP6/T7,
XX for the human heavy chain J region. Anti-CD4 antibodies may be used in
XX therapeutic and diagnostic applications, especially for the treatment
XX of human diseases. These antibodies reduce activity of CD4 cells and
XX reduce undesirable autoimmune reactions, inflammatory response and
XX transplant rejection. Transgenic animals are capable of producing
XX heterologous antibodies of multiple isotypes by undergoing isotype
XX switching. These animals produce a first Ig type that is necessary for
XX antigen-stimulated B-cell maturation and can switch to encode and
XX produce one or more subsequent heterologous isotypes.
XX
XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

```

```

PI Kay RM, Lonberg N;
XX
XX WPI; 1997-235888/21.
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
XX treatment of auto-immune disease etc.
XX
XX Example 12; Page 133; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply
XX 100000000 M-1 for binding to a predetermined human antigen. The
XX present sequence represents a probe used to screen a human placental
XX genomic DNA library cloned into the phage vector lambdaEMBL3/SP6/T7,
XX for the human heavy chain J region. Anti-CD4 antibodies may be used in
XX therapeutic and diagnostic applications, especially for the treatment
XX of human diseases. These antibodies reduce activity of CD4 cells and
XX reduce undesirable autoimmune reactions, inflammatory response and
XX transplant rejection. Transgenic animals are capable of producing
XX heterologous antibodies of multiple isotypes by undergoing isotype
XX switching. These animals produce a first Ig type that is necessary for
XX antigen-stimulated B-cell maturation and can switch to encode and
XX produce one or more subsequent heterologous isotypes.
XX
XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| |||||
DB 35 CCAGACATCAAAAGCATCAC 16

RESULT 15
AAT73448/C
ID AAT73448 standard; DNA; 42 BP.
XX
XX AAT73448;
XX
XX 03-DEC-1997 (first entry)
XX
XX Human J-mu region genomic DNA library probe.
XX
XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
XX transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
XX transplant rejection; ss.
XX
XX Synthetic.
XX
XX WO9713852-A1.
XX
XX 17-APR-1997.
XX
XX 10-OCT-1996; 96WO-US16433.
XX
XX 10-OCT-1995; 95US-0544404.
XX
XX (GENP-) GENPHARM INT INC.
XX
XX Kay RM, Lonberg N;
XX
XX WPI; 1997-235888/21.
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
XX treatment of auto-immune disease etc.
XX
XX Example 4; Page 103; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply

```

CC 1000000000 M-1 for binding to a predetermined human antigen. The  
CC present sequence represents a probe used for the isolation of human  
CC J segments from a human genomic DNA library. The anti-CD4 antibodies  
CC may be used in therapeutic and diagnostic applications, especially for  
CC the treatment of human diseases. These antibodies reduce activity of  
CC CD4 cells and reduce undesirable autoimmune reactions, inflammatory  
CC response and transplant rejection. Transgenic animals are capable of  
CC producing heterologous antibodies of multiple isotypes by undergoing  
CC isotype switching. These animals produce a first Ig type that is  
CC necessary for antigen-stimulated B-cell maturation and can switch to  
CC encode and produce one or more subsequent heterologous isotypes.

XX  
SQ Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 42;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
|||  
Db 35 CCAGACATCAAAAGCATCAC 16

Search completed: October 2, 2001, 16:18:41  
Job time: 15485 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:49 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100b-11

Perfect score: 20

Sequence: 1 agtaccagggtgagctcttag 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCRUS.COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-377-310-11
2	15	75.0	15	3	US-09-377-310-31
c 3	13.4	67.0	21	1	US-08-136-118-7
c 4	12.8	64.0	27	4	US-09-246-277A-8
c 5	12.8	64.0	29	1	US-08-530-492-69
c 6	12.8	64.0	29	4	US-08-906-517-69
7	12.8	64.0	34	2	US-08-988-128-15
c 8	12.8	64.0	48	2	US-08-865-675-6
c 9	12.8	64.0	48	2	US-09-237-510-6
c 10	12.4	62.0	20	4	US-09-488-671-119
c 11	12.4	62.0	22	2	US-08-117-952-668
c 12	12.4	62.0	46	4	US-09-060-410-12
c 13	12.2	61.0	20	4	US-09-101-886B-71
14	12.2	61.0	32	3	US-08-685-871-14
15	12.2	61.0	32	3	US-08-685-871-27
16	12.2	61.0	32	3	US-08-685-871-31
17	12.2	61.0	32	3	US-08-685-871-33
18	12.2	61.0	32	3	US-08-685-871-41
19	12.2	61.0	32	3	US-08-685-871-43
c 20	12.2	61.0	44	2	US-07-916-098A-36
21	12.2	61.0	44	2	US-07-916-098A-59
22	12	60.0	20	2	US-08-609-443B-53
c 23	12	60.0	30	3	US-09-339-993-4
c 24	11.8	59.0	20	3	US-09-257-799-49
25	11.8	59.0	20	3	US-08-920-919A-49
26	11.8	59.0	41	2	US-08-818-604-8
c 27	11.6	58.0	26	1	US-08-482-882-87

c 28	11.6	58.0	26	1	US-08-483-389-87	Sequence 87, Appl
c 29	11.6	58.0	26	2	US-08-487-113D-87	Sequence 87, Appl
c 30	11.6	58.0	26	2	US-08-473-503-87	Sequence 87, Appl
c 31	11.6	58.0	26	2	US-08-483-932-87	Sequence 87, Appl
c 32	11.6	58.0	26	2	US-08-720-420A-87	Sequence 87, Appl
c 33	11.6	58.0	26	2	US-08-859-998-95	Sequence 95, Appl
c 34	11.6	58.0	26	3	US-08-714-017-87	Sequence 87, Appl
c 35	11.6	58.0	26	3	US-08-475-680-87	Sequence 87, Appl
c 36	11.6	58.0	40	1	US-08-482-882-100	Sequence 100, App
c 37	11.6	58.0	40	1	US-08-483-389-100	Sequence 100, App
c 38	11.6	58.0	40	2	US-08-487-113D-100	Sequence 100, App
c 39	11.6	58.0	40	2	US-08-473-503-100	Sequence 100, App
c 40	11.6	58.0	40	2	US-08-483-932-100	Sequence 100, App
c 41	11.6	58.0	40	2	US-08-720-420A-100	Sequence 100, App
c 42	11.6	58.0	40	3	US-08-714-017-100	Sequence 100, App
c 43	11.6	58.0	40	3	US-08-475-680-100	Sequence 100, App
c 44	11.6	58.0	42	1	US-07-834-539A-58	Sequence 58, Appl
c 45	11.6	58.0	42	5	PCT-US92-10983-106	Sequence 106, App

ALIGNMENTS

RESULT 1  
US-09-377-310-11  
; Sequence 11, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-11

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 agtaccagggtgagctcttag 20  
|||||  
Db 1 agtaccagggtgagctcttag 20

RESULT 2  
US-09-377-310-31  
; Sequence 31, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-31

Query Match      75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccagggtgagct 17
   |||||
Db 1 taccagggtgagct 15

RESULT 3
US-08-136-118-7/c
; Sequence 7, Application US/08136118
; Patent No. 5580969
; GENERAL INFORMATION:
; APPLICANT: HOKE, Glenn D
; APPLICANT: BRADLEY, Matthews O
; APPLICANT: WILLIAMS, Taffy J
; APPLICANT: LEE, Che-Hung
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED
; AGAINST HUMAN ICAM-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; STREET: 8901 Naval Medical Res. & Dev. Cmd.
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/136,118
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/918,259
; FILING DATE: 24-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Spevack, A. David
; REGISTRATION NUMBER: 24,743
; REFERENCE/DOCKET NUMBER: N.C. 75,776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 295-6759
; TELEFAX: (202) 295-1022
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-136-118-7

Query Match      67.0%; Score 13.4; DB 1; Length 21;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 gtaccagggtgagtc 16
   |||||
Db 19 GTTCCCGAGGTGAGTC 5

RESULT 4
US-09-246-277A-8/c
; Sequence 8, Application US/09246277A
; Patent No. 6238866
; GENERAL INFORMATION:
; APPLICANT: Yeh, Homer R., Wick, Charles H.
; TITLE OF INVENTION: NOVEL DETECTOR FOR NUCLEIC ACID
; TYPING AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of the Chief Counsel
; STREET: U.S. Army SBCCOM
; CITY: APG(EA)
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/246,277A
; FILING DATE: 08-Feb-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. John
; REGISTRATION NUMBER: 39908
; REFERENCE/DOCKET NUMBER: 436-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (410) 436-1158
; TELEFAX: (410) 436-2534
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: EFD52 Minisatellite
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-246-277A-8

Query Match      64.0%; Score 12.8; DB 4; Length 27;
Best Local Similarity 70.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagcttag 20
   |||||
Db 22 AGTARCCAGGRSWGTCGTAG 3

RESULT 5
US-08-530-492-69/c
; Sequence 69, Application US/08530492
; Patent No. 5689052
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Dean, Duff A.
; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; Expression in Monocotyledonous Plants and Method For
; Preparation Thereof
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Parkway No. 5689052th
```



CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/530,492  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/172,333  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10605)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6099  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-530-492-69

Query Match 64.0%; Score 12.8; DB 1; Length 29;  
Best Local Similarity 87.5%; Pred. No. 2.5e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagtc 16  
||| ||||| |||||  
Db 24 AGTCCCCAGGAGAGTC 9

RESULT 6  
US-08-906-517-69/c  
Sequence 69, Application US/08906517  
Patent No. 6180774  
GENERAL INFORMATION:  
APPLICANT: Brown, Sherri M.  
APPLICANT: Dean, Duff A.  
APPLICANT: Fromm, Michael E.  
APPLICANT: Sanders, Patricia R.  
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced  
TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For  
TITLE OF INVENTION: Preparation Thereof  
NUMBER OF SEQUENCE ADDRESSES: 164  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,517  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT:170  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-418-3000  
TELEFAX: 512-474-7577 69:  
INFORMATION FOR SEQ ID NO:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-906-517-69

Query Match 64.0%; Score 12.8; DB 4; Length 29;  
Best Local Similarity 87.5%; Pred. No. 2.5e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagtc 16  
||| ||||| |||||  
Db 24 AGTCCCCAGGAGAGTC 9

RESULT 7  
US-08-988-128-15  
Sequence 15, Application US/08988128  
Patent No. 5994505  
GENERAL INFORMATION:  
APPLICANT: Ting, Jenny Pan-Yung  
APPLICANT: Chin, Keh-Chin  
TITLE OF INVENTION: No. 5994505el Forms of Class II MHC  
TITLE OF INVENTION: Transactivator (CIITA)  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Myers Bigel Sibley & Sajovec, P.A.  
STREET: P.O. Box 37428  
CITY: Raleigh  
STATE: No. 5994505th Carolina  
COUNTRY: USA  
ZIP: 27627  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,128  
FILING DATE: 10-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Biswas, Sorojini J.  
REGISTRATION NUMBER: 39,111  
REFERENCE/DOCKET NUMBER: 5470-136  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 854-1400  
TELEFAX: (919) 854-1401  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-988-128-15

Query Match 64.0%; Score 12.8; DB 2; Length 34;  
Best Local Similarity 87.5%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 taccagggtgagtcctt 18  
||| ||||| ||| |||||  
Db 16 TACCAGCTGTGTCTT 31



STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,952  
FILING DATE: 07-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,471  
FILING DATE: 15-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9423  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 668:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Oligonucleotide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-117-952-668

Query Match 62.0%; Score 12.4; DB 2; Length 22;  
Best Local Similarity 92.9%; Pred. No. 4e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 acccaggtgagtct 17  
| |||||  
DB 14 ATCCAGGTGAGTCT 1

RESULT 12  
US-09-060-410-12/c  
Sequence 12, Application US/09060410  
Patent No. 6165461  
GENERAL INFORMATION:  
APPLICANT: Cobb, Melanie  
APPLICANT: Hutchinson, Michele  
APPLICANT: Chen, Zhu  
APPLICANT: Berman, Kevin  
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,410  
FILING DATE: 14-APR-1998  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.421  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-060-410-12  
Query Match 62.0%; Score 12.4; DB 4; Length 46;  
Best Local Similarity 92.9%; Pred. No. 4.4e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 agtaccaggtgag 14  
| |||||  
DB 14 AGTACCCAGGTGAG 1  
RESULT 13  
US-09-101-886B-71  
Sequence 71, Application US/09101886B  
Patent No. 6197507  
GENERAL INFORMATION:  
APPLICANT: BERG, THOMAS  
APPLICANT: TOLLERSKUD, OLE K  
APPLICANT: NILSEN, OIVIND  
TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BARBARA G. ERNST  
STREET: 555 13TH STREET, NW SUITE 701E  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/101,886B  
FILING DATE: 29-JANUARY-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB97/00109  
FILING DATE: 12-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, BARBARA G  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1181-240  
TELEPHONE: 202-783-6040  
TELEFAX: 202-783-6031  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-101-886B-71

Query Match 61.0%; Score 12.2; DB 4; Length 20;  
Best Local Similarity 82.4%; Pred. No. 5.1e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccaggtgagctt 17  
| | ||||| | | | | |  
Db 2 AATGCCAGGTGAGTGT 18

RESULT 14  
US-08-685-871-14  
; Sequence 14, Application US/08685871  
; Patent No. 6013499  
; GENERAL INFORMATION:  
; APPLICANT: NARUMIYA, Shuh  
; APPLICANT: IWAMATSU, Akihiro  
; TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685.871  
; FILING DATE: 24-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-184102  
; FILING DATE: 25-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-262553  
; FILING DATE: 14-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16887/845  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-685-871-14

Query Match 61.0%; Score 12.2; DB 3; Length 32;  
Best Local Similarity 82.4%; Pred. No. 5.4e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 acccaggtgagctcttag 20  
| | | | | | | | | |  
Db 3 ACCCGGGTGTGTATTAG 19

RESULT 15  
US-08-685-871-27  
; Sequence 27, Application US/08685871  
; Patent No. 6013499  
; GENERAL INFORMATION:  
; APPLICANT: NARUMIYA, Shuh  
; APPLICANT: IWAMATSU, Akihiro

; TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685.871  
; FILING DATE: 24-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-184102  
; FILING DATE: 25-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-262553  
; FILING DATE: 14-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16887/845  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-685-871-27

Query Match 61.0%; Score 12.2; DB 3; Length 32;  
Best Local Similarity 82.4%; Pred. No. 5.4e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 acccaggtgagctcttag 20  
| | | | | | | | | |  
Db 3 ACCCGGGTGTGTATTAG 19

Search completed: October 2, 2001, 16:03:49  
Job time: 14593 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:39 ; Search time 876.95 Seconds  
(without alignments)  
14.320 Million cell updates/sec

Title: US-09-757-100B-11

Perfect score: 20

Sequence: 1 agtaccaggtagctcttag 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
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5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65543 Human focal adhesi
2	15	75.0	15	22	AAC65563 Human focal adhesi
3	13.4	67.0	21	18	AA758077 ICAM-1 antisense o
4	13.4	67.0	21	19	AAV38613 Human ICAM-1, E-se
5	13.2	66.0	36	22	AAAF92420 Pro alpha 2 (f) co
6	12.8	64.0	23	21	AAAF10299 HIV-1 LTR (long te
7	12.8	64.0	25	21	AAAF2481 Soybean chalcone r
8	12.8	64.0	29	19	AAV00357 Bacillus thuringie
9	12.8	64.0	29	22	AAAF3275 Oligonucleotide #6
10	12.8	64.0	34	19	AAV15306 Primer for adeno-a
11	12.8	64.0	48	20	AAV82665 Target oligonucleo

C 12	12.4	62.0	20	22	AAF62963 Mouse PEPCCK-cytoso
C 13	12.4	62.0	22	16	AAO82668 Chromosome 11 (loc
C 14	12.4	62.0	33	16	AAO86221 GC PCR primer #2.
15	12.4	62.0	33	16	AAO86223 GC PCR (R) primer
16	12.4	62.0	33	16	AAO86223 Glucocerebrosidase
17	12.4	62.0	33	22	AAF98212 C neoformans strai
C 18	12.4	62.0	46	20	AAZ32444 Human retina EST T
C 19	12.2	61.0	28	17	AAZ35702 3' VH primer VHTp3
20	12.2	61.0	32	18	AAZ35702 Physiologically ac
21	12.2	61.0	32	18	AAZ35702 Physiologically ac
22	12.2	61.0	32	18	AAZ35702 Physiologically ac
23	12.2	61.0	32	18	AAZ35702 Physiologically ac
24	12.2	61.0	32	18	AAZ35702 Physiologically ac
25	12.2	61.0	32	18	AAZ35702 Physiologically ac
26	12.2	61.0	32	18	AAZ35702 Physiologically ac
27	12.2	61.0	32	18	AAZ35702 Physiologically ac
28	12.2	61.0	32	19	AAV43407 3' PCR primer used
C 29	12.2	61.0	44	13	AAQ30902 Oligonucleotide 31
30	12.2	61.0	44	13	AAQ30922 Oligonucleotide 31
31	12	60.0	20	17	AAZ37941 VEGF-B186 exon 5 b
32	12	60.0	20	17	AAZ37941 VEGF-B167 exon 5 b
33	12	60.0	20	19	AAV28523 Blackcurrant rever
34	12	60.0	20	20	AAV63604 Human VEGF-B186 ex
C 35	12	60.0	21	20	AAZ35657 PCR primer used to
C 36	12	60.0	21	21	AAZ35657 PCR primer hpl-690
C 37	12	60.0	22	22	AAZ35657 Human heparanase.
38	12	60.0	23	21	AAZ35657 Heparanase express
39	12	60.0	23	21	AAZ35657 V-gamma 1.4 sequen
C 40	12	60.0	27	13	AAQ24751 PCR primer for CDN
41	12	60.0	27	20	AAZ35657 probe specific for
C 42	12	60.0	30	21	AAZ35657 Human ST receptor
C 43	12	60.0	32	19	AAZ35657 Single base extens
C 44	12	60.0	41	21	AAZ35657 Hammerhead ribozym
C 45	11.8	59.0	17	21	AAZ35657

ALIGNMENTS

RESULT 1  
AAC65543 AAC65543 standard; DNA; 20 BP.  
ID AAC65543  
AC AAC65543;  
XX AAC65543;  
XX AAC65543;  
DT 12-FEB-2001 (first entry)  
XX 12-FEB-2001 (first entry)  
DE Human focal adhesion kinase antisense sequence #9.  
XX Human; focal adhesion kinase; FAK; signal transduction; cancer;  
KW embryonic development disorder; angiogenic disorder; wound healing;  
KW antisense; phosphorothioate; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Homo sapiens.  
PN US6133031-A.  
XX US6133031-A.  
PD 17-OCT-2000.  
XX 17-OCT-2000.  
PF 19-AUG-1999; 99US-0377310.  
XX 19-AUG-1999; 99US-0377310.  
PR 19-AUG-1999; 99US-0377310.  
XX (ISIS-) ISIS PHARM INC.  
PA Monia BP, Gaarde WA;  
PI Monia BP, Gaarde WA;  
DR WPI; 2001-006141/01.  
XX New antisense compounds for inhibiting focal adhesion kinase  
PT expression, especially useful for inhibiting retinal  
XX neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Claim 15; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
CC is involved in integrin-mediated signal transduction, and is implicated  
CC in cancer, particularly colon, breast and oral tumours, embryonic  
CC development disorders, angiogenic disorders and wound healing. The  
CC antisense sequences, including the one shown here, can be used in the  
CC treatment of all of these.

XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agtaccaggtgagttcttag 20

|||||

Db 1 agtaccaggtgagttcttag 20

RESULT 2

AAC65563

ID AAC65563 standard; DNA; 15 BP.

XX

AC AAC65563;

DT 12-FEB-2001 (first entry)

XX

DE Human focal adhesion kinase antisense sequence #29.

XX

KW Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX

OS Homo sapiens.

XX

PN US6133031-A.

XX

PD 17-OCT-2000.

XX

PF 19-AUG-1999; 99US-0377310.

XX

PR 19-AUG-1999; 99US-0377310.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Gaarde WA;

XX

DR WPI; 2001-006141/01.

XX

PT New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX

PS Claim 15; Column 25; 30pp; English.

XX

CC The present invention describes a number of phosphorothioate antisense

CC sequences to the human focal adhesion kinase (FAK) protein. This protein

CC is involved in integrin-mediated signal transduction, and is implicated

CC in cancer, particularly colon, breast and oral tumours, embryonic

CC development disorders, angiogenic disorders and wound healing. The

CC antisense sequences, including the one shown here, can be used in the

CC treatment of all of these.

XX

XX Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 75.0%; Score 15; DB 22; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccacagtgagtct 17

|||||

Db 1 taccacagtgagtct 15

RESULT 3

AAT58077/C

ID AAT58077 standard; DNA; 21 BP.

XX

AC AAT58077;

XX

DT 18-MAR-1997 (first entry)

XX

DE ICAM-1 antisense oligonucleotide #7.

XX

KW Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect;

KW human intercellular adhesion molecule-1; ICAM-1; inflammation;

KW adult respiratory distress syndrome; multiple organ failure; GM1594;

KW septic shock; ss.

XX

OS Synthetic.

XX

PN US5580969-A.

XX

PD 03-DEC-1996.

XX

PF 24-JUL-1992; 92US-0918259.

XX

PR 12-OCT-1993; 93US-0136118.

XX

PR 24-JUL-1992; 92US-0918259.

XX

PA (USNA ) US SEC OF NAVY.

XX

PI Bradley MO, Hoke GD, Lee C, Williams TJ;

XX

DR WPI; 1997-033603/03.

XX

PT Anti-sense oligo:nucleotide(s) for blocking ICAM-1 mRNA translation

PT - for treating septic shock, adult respiratory distress syndrome

PT etc.

XX

PS Claim 1; Column 21; 16pp; English.

XX

CC The sequences given in AAT58071-85 represent oligonucleotides which are

CC antisense to sequences contained in the pre-mRNA or mature mRNA

CC transcript of human intercellular adhesion molecule-1 (ICAM-1).

CC These oligonucleotides may be used for treating septic shock and the

CC manifestations of septic shock, e.g. inflammation, and vascular and

CC tissue defects. They are also useful in the treatment of septic

CC shock associated diseases, e.g. adult respiratory distress syndrome,

CC multiple organ failure etc.

XX

SQ Sequence 21 BP; 5 A; 9 C; 5 G; 2 T; 0 other;

Query Match

Best Local Similarity 67.0%; Score 13.4; DB 18; Length 21;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 gtaccacagtgagtc 16

|||||

Db 19 GTTCCCGAGTGAGTC 5

RESULT 4

AAV38613/C

ID AAV38613 standard; DNA; 21 BP.

XX

AC AAV38613;

XX

DT 13-OCT-1998 (first entry)

XX

DE Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.



```

XX ICAM-1; intracellular adhesion molecule-; E-selectin; VCAM-1;
KW vascular cell adhesion molecule-1; antisense; inflammatory;
KW disease; treatment; septic shock; psoriasis; wounds; burns; acne;
KW arthritis; organ rejection; inhibition; expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN WO9824797-A1.
XX
PD 11-JUN-1998.
XX
XX 02-DEC-1996; 96WO-US19194.
XX
XX 02-DEC-1996; 96WO-US19194.
XX
XX (DYAD-) DYAD PHARM CORP.
XX
XX Bradley MO, Hoke GD, Lee C, Williams TJ;
XX WPI; 1998-333253/29.
XX
XX Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful
PT for treating diseases having an inflammatory component, e.g.
PT psoriasis, wounds and septic shock
XX
XX Claim 8; Page 40; 48pp; English.
XX
XX The sequence is that of an antisense oligonucleotide which is
CC substantially complementary to at least a portion of the pre-
CC or mature RNA transcript of human intracellular adhesion molecule
CC (ICAM), E-selectin or vascular cell adhesion molecule (VCAM).
CC It can be used to inhibit expression of these proteins. Inhibition
CC of these proteins forms the basis for treatment of conditions and
CC diseases that have an inflammatory component, e.g. acne, psoriasis,
CC arthritis, organ rejection, wounds, burns, septic shock or
CC inflammatory complications of septic shock.
XX
XX Sequence 21 BP; 5 A; 9 C; 5 G; 2 T; 0 other;
SQ
Query Match 67.0%; Score 13.4; DB 19; Length 21;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 gtacccaggtagtc 16
DB || ||||| |||||
19 GTTCCAGGTGAGTC 5
RESULT 5
AAF92420
ID AAF92420 standard; DNA; 36 BP.
XX
XX AAF92420;
XX
XX 16-MAY-2001 (first entry)
XX
XX Pro alpha 2 (I) collagen (COL1A2) specific PCR primer SEQ ID 65.
XX
XX Human; cytochrome P450; Cyp3A; PCR primer; transgenic mouse;
KW immortalised cell; ss.
XX
XX Homo sapiens.
XX
XX WO200111951-A1.
XX
XX 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-JP05424.
XX
XX 13-AUG-1999; 99JP-0229094.

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XX (KIRI ) KIRIN BEER KK.
PA
XX Ishida I, Tomizuka K, Kuroiwa Y, Ohshima T, Suzuki M, Itoh K;
PI
XX WPI; 2001-202806/20.
DR
XX
XX Mouse having completely humanized human cytochrome P450 gene for use in
PT studying drug efficacy, metabolism and toxicity with ease -
PT
XX Example 16; Page 67; 137pp; Japanese.
XX
XX This invention relates to a mouse containing the human cytochrome P450
CC gene (from the CYP3A family). PCR primers AAF92356 - AAF92441 are used
CC in examples illustrating the construction of vectors used in the
CC production of the transgenic mouse of the invention. The mouse can be
CC used for studying human drug efficacy, metabolism and toxicity, including
CC the application of immortalised cell and tissue cultures.
XX
XX Sequence 36 BP; 8 A; 7 C; 8 G; 13 T; 0 other;
SQ
Query Match 66.0%; Score 13.2; DB 22; Length 36;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 gtacccaggtagtcctta 19
DB ||||| || || |||
6 gtacccaggtagtcaggctta 23
RESULT 6
AAAl0299
ID AAAl0299 standard; DNA; 23 BP.
XX
XX AAAl0299;
XX
XX 03-JUL-2000 (first entry)
XX
XX HIV-1 LTR (long terminal repeat) PCR primer, SEQ ID NO:4.
XX
XX Long terminal repeat; LTR; HIV-1; APJ receptor; coreceptor;
KW cellular infection; envelope protein; env; CD4 coexpression;
KW drug development; PCR primer; ss.
XX
XX Human immunodeficiency virus type 1.
OS
XX WO200014220-A1.
XX
XX 16-MAR-2000.
XX
XX 07-SEP-1999; 99WO-EP06553.
XX
XX 08-SEP-1998; 98US-0149045.
XX
XX (SCHD ) SCHERING AG.
XX
XX Doms R, Faulds D, Hesselgesser JE, Horuk R, Mitrovic B, Zhou Y;
PI
XX WPI; 2000-256972/22.
XX
XX New recombinant eukaryotic cells coexpressing APJ and CD4 polypeptides,
PT useful for identifying compounds that modulate interaction between an
PT HIV virus and an APJ receptor e.g. to develop anti-HIV drugs -
XX
XX Example 2; Page 36; 67pp; English.
XX
XX The invention relates to recombinant eukaryotic cells transformed with a
CC nucleotide encoding an APJ protein and/or a nucleotide encoding the CD4
CC protein, such that the cells coexpress APJ and CD4. The APJ receptor
CC (AAyB/466) is an orphan seven transmembrane domain receptor that has
CC been found to function as an efficient coreceptor for cellular infection
CC by a number of HIV-1 and SIV strains. The entry of HIV into cells

```

CC involves binding of the viral envelope protein (env) to CD4, followed by  
 CC interaction with a coreceptor. Binding to the coreceptor triggers a  
 CC conformational change in env that mediates fusion between the viral  
 CC membrane and the host cell membrane. The invention also encompasses  
 CC peptides and antibodies which specifically bind to an extracellular  
 CC domain of APJ. These inhibit membrane fusion between a cell coexpressing  
 CC the APJ and CD4 proteins and a cell expressing an HIV env protein and  
 CC thereby inhibits HIV infection of the APJ/CD4-expressing cell. The new  
 CC recombinant cells provide an important tool for investigating and  
 CC that modulate interaction between HIV and an APJ receptor, which may be  
 CC useful in the development of anti-HIV drugs. Contacting cells expressing  
 CC APJ and CD4 with an APJ binding/blocking agent (e.g., the antibodies or  
 CC peptides) may be useful to inhibit HIV infection of such cells, e.g., to  
 CC treat subjects having an HIV-related disorder associated with APJ  
 CC expression. Antibodies and peptide fragments can be included in  
 CC medicines and administered to treat patients (especially foetuses)  
 CC having, or at risk of developing, an HIV infection or related disorder.  
 CC The antibodies can also be used to detect cells expressing the APJ receptor,  
 CC and are useful to diagnose susceptibility to HIV infection. For example,  
 CC higher APJ levels in central nervous system tissues may indicate an  
 CC increased risk of neurodegeneration associated with HIV infection.  
 CC Transgenic animals which express human CD4 and APJ proteins may provide  
 CC model systems for the study of HIV infection and for anti-HIV drug  
 CC development. Sequences AAA10299-A10300 represent PCR primers used in an  
 CC exemplification of the present invention to amplify HIV-1 LTR (long  
 CC terminal repeat) DNA sequences from CD4/APJ-expressing cells which had  
 CC been previously exposed to HIV-1. The amplified LTR DNA was detected via  
 CC hybridisation with a labelled probe (AAA10301).  
 XX  
 SQ Sequence 23 BP; 7 A; 7 C; 5 G; 4 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 23;  
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 agtaccagggtgagtc 16  
 ||||| |||||  
 Db 8 agtaccagggtgagtc 23

RESULT 7  
 AAA72481/c  
 ID AAA72481 standard; DNA; 25 BP.  
 XX  
 AC AAA72481;  
 XX  
 DT 19-DEC-2000 (first entry)  
 DE  
 DE Soybean chalcone reductase PCR primer, SEQ ID NO:65.  
 XX  
 KW Soybean; chalcone reductase; phenylpropanoid pathway;  
 KW isoflavone synthase; isoflavonoid biosynthesis; defence response;  
 KW attractant; repellent; signal compound; antibiotic; transgenic plant;  
 KW transgenic seed; PCR primer; ss.  
 OS  
 OS Glycine max.  
 XX  
 PN WO200044909-A1.  
 XX  
 PD 03-AUG-2000.  
 XX  
 PF 26-JAN-2000; 2000WO-US01772.  
 XX  
 PR 27-JAN-1999; 99US-0117769.  
 PR 20-JUL-1999; 99US-0144783.  
 PR 24-SEP-1999; 99US-0156094.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Fader GM, Jung W, McGonigle B, Odell JT, Yu X;  
 XX

DR WPI; 2000-543395/49.  
 XX Nucleic acids encoding isoflavonoid synthases, useful for producing  
 PT transgenic plants with increased production of isoflavonoids which are  
 PT involved in defense against phytopathogenic microorganisms -  
 XX Example 14; Page 52; 157pp; English.  
 XX Sequences AAA72437, AAA72449-A72461, AAA72468 and AAA72474-A72477  
 CC represent cDNAs encoding novel plant isoflavone synthases (AAB21052 and  
 CC AAB21054 - AAB21071). Also disclosed is the soybean cytochrome P450  
 CC monooxygenase CYP93C1, encoded by a known sequence (AAA72444, NCBI No.  
 CC 2739005), which was identified in the present invention as having  
 CC isoflavone synthase activity. The invention also relates to expression  
 CC constructs, transformed host cells, and transgenic plants and seeds  
 CC comprising the novel cDNA sequences of the invention. The invention also  
 CC encompasses methods of altering isoflavone synthase expression in a host  
 CC cell, altering isoflavonoid levels in a plant, and identifying nucleic  
 CC acids encoding other plant isoflavone synthases. Isoflavone synthase  
 CC plays a key role in the biosynthesis of isoflavonoids. Isoflavonoids are  
 CC a class of secondary metabolites mainly produced in leguminous plants by  
 CC a branch of the phenylpropanoid pathway. Isoflavone synthase catalyses  
 CC the first step in the branch of this pathway that commits metabolic  
 CC intermediates to the synthesis of isoflavonoids. Isoflavonoids  
 CC participate in the defence response of legumes against phytopathogenic  
 CC microorganisms and are also involved in symbiotic relationships between  
 CC the roots of legumes and rhizobial bacteria which eventually result in  
 CC nodulation and nitrogen-fixation. They have also been shown to act as  
 CC antibiotics, repellents, attractants, and signal compounds, and  
 CC consumption of legume isoflavonoids is associated with health benefits  
 CC in humans. The novel isoflavonoid synthases, and nucleic acids encoding  
 CC them, are useful for altering the levels of isoflavonoids produced in  
 CC legumes such as soybean, and for the production of isoflavonoids in  
 CC plants which do not naturally produce them (e.g., maize, rice, wheat).  
 CC Sequences AAA72478-A72481 represent PCR primers used in an  
 CC exemplification of the invention to amplify DNA encoding soybean chalcone  
 CC reductase (an enzyme that acts upstream of isoflavone synthase in the  
 CC phenylpropanoid pathway).  
 XX  
 SQ Sequence 25 BP; 6 A; 7 C; 5 G; 7 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 25;  
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cccagggtgagtccttag 20  
 ||||| ||||| |||||  
 Db 17 CCCAGGTGAGTTTGAG 2

RESULT 8  
 AAV00357/c  
 ID AAV00357 standard; DNA; 29 BP.  
 XX  
 AC AAV00357;  
 XX  
 DT 23-APR-1998 (first entry)  
 DE  
 DE Bacillus thuringiensis insecticidal gene modification primer BTK58.  
 XX  
 KW Insecticidal protein; Bacillus thuringiensis; monocotyledonous plant;  
 KW structural gene; maize; CryI(b); CryIIb; primer; ss.  
 XX  
 OS Synthetic.  
 OS Bacillus thuringiensis.  
 XX  
 PN US5689052-A.  
 XX  
 PD 18-NOV-1997.  
 XX  
 PF 19-SEP-1995; 95US-0530492.  
 XX

PR 22-DEC-1993; 93US-0172333.  
PR 19-SEP-1995; 95US-0530492.  
PA (MONS ) MONSANTO CO.  
XX Brown SM, Dean DA, Fromm ME, Sanders PR;  
XX WPI; 1998-008070/01.  
XX Genes encoding insecticidal proteins of *Bacillus thuringiensis* -  
PT modified to enhance expression in monocotyledonous plants  
XX Example 1; Column 17; 86pp; English.  
XX The present sequence represents a primer used in the present invention  
CC describing new structural genes capable of being expressed in a  
CC monocotyledonous plant. The new genes comprise modified nucleotide  
CC sequences which encode insecticidal proteins of *Bacillus thuringiensis*.  
CC The genes have been modified to reduce the usage of codons that are  
CC rare or semi-rare in monocotyledon DNA, thereby increasing  
CC transformation efficiency and/or increasing accumulation of the  
CC insecticidal protein in monocotyledon tissues.  
XX Insecticidal protein in monocotyledon tissues.  
XX Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 other;  
SQ

Query Match 64.0%; Score 12.8; DB 19; Length 29;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agtaccaggtagtc 16  
||| ||||| |||||  
DB 24 AGTCCCCAGGAGATC 9

RESULT 9  
AAE73275/c  
ID AAE73275 standard; DNA; 29 BP.  
XX  
AC AAE73275;  
XX  
DT 26-APR-2001 (first entry)  
XX  
DE Oligonucleotide #66.  
XX  
XX CRYIA; transgenic; crystal; toxin; insecticide; ss.  
XX Synthetic.  
XX  
XX US6180774-B1.  
XX  
XX 30-JAN-2001.  
XX  
XX 05-AUG-1997; 97US-0906517.  
XX  
XX 19-SEP-1995; 95US-0530492.  
XX  
XX 22-DEC-1993; 93US-0172333.  
XX  
XX (MONS ) MONSANTO CO.  
XX  
XX Brown SM, Dean DA, Fromm ME, Sanders PR;  
XX WPI; 2001-190861/19.  
XX  
XX Novel nucleic acids, useful for transgenic plant production which is  
PT capable of expressing increased levels of desired proteins -  
XX  
XX Example 1; Column 16; 81pp; English.  
XX  
XX The present invention relates to nucleotides 669-1348 of a  
CC *B.thuringiensis* CryIA(b). The invention is useful for transgenic  
CC plant production, e.g. maize, capable of expressing increased  
CC amount of transgenic protein, e.g. crystal protein toxin gene

CC of *Bacillus thuringiensis*.  
XX Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 other;  
SQ

Query Match 64.0%; Score 12.8; DB 22; Length 29;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agtaccaggtagtc 16  
||| ||||| |||||  
DB 24 AGTCCCCAGGAGATC 9

RESULT 10  
AAV15506  
ID AAV15506 standard; DNA; 34 BP.  
XX  
AC AAV15506;  
XX  
DT 11-JUN-1998 (first entry)  
XX  
XX Primer for adeno-associated virus DNA.  
XX  
XX AAV; vector; rep 68/78; PCR primer; gene therapy; ss.  
XX Synthetic.  
XX Adeno associated virus.  
XX  
XX WO9749824-A1.  
XX  
XX 31-DEC-1997.  
XX  
XX 24-JUN-1997; 97WO-DE01333.  
XX  
XX 24-JUN-1996; 96DE-1025188.  
XX  
XX (MEDI-) MEDIGENE GMBH.  
XX (MEDI-) MEDIGENE AG.  
XX  
XX Bogedain C, Hallek M, Maass G;  
XX WPI; 1998-086641/08.  
XX  
XX System of adeno-associated viral vector and rep 68/78 sequence of  
PT this virus- expression of which is delayed until replication of  
PT viral DNA has started, provides large scale production of vectors  
PT for gene therapy  
XX  
XX Example; Page 7; 20pp; German.  
XX  
XX The present sequence was used in the development of a novel system,  
CC comprising an adeno-associated virus (AAV) vector containing a  
CC foreign DNA, and the rep 68/78 sequence of AAV, the expression of  
CC which is delayed. The components may be present in cis (in a single  
CC agent) or in trans (in separate agents).  
CC The system is used for production of AAV vectors, particularly for  
CC gene therapy. The foreign DNA may encode a therapeutic factor or  
CC e.g. interferon, interleukin, growth factor, coagulation protein or  
CC metabolic enzyme, particularly one that increases the  
CC immunogenicity of tumour cells, and/or a diagnostic protein. The  
CC system produces AAV vectors on a large scale. It is based on the  
CC discovery that the rep68 and 78 proteins interfere with replication  
CC of AAV DNA, and that this interference is overcome by delaying  
CC expression of these proteins.  
XX  
XX Sequence 34 BP; 4 A; 13 C; 9 G; 8 T; 0 other;  
SQ

Query Match 64.0%; Score 12.8; DB 19; Length 34;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gtaccaggtagtct 17  
 ||| ||| ||| |||  
 Db 5 gtaccaggtagtct 20

RESULT 11  
 AAV82665/C  
 ID AAV82665 standard; DNA; 48 BP.

XX AC AAV82665;

XX DT 25-FEB-1999 (first entry)

XX DE Target oligonucleotide JN5.

XX KW Detector oligonucleotide; hairpin structure; fluorescence;

XX KW primer extension; hybridization; signal primer; frameshift mutation;  
 ss.

XX OS Synthetic.

XX PN EP881302-A2.

XX PD 02-DEC-1998.

XX PF 28-MAY-1998; 98EP-0109682.

XX PR 30-MAY-1997; 97US-0865675.

XX PA (BECT ) BECTON DICKINSON & CO.

XX PI Linn PC, Nadeau JG, Pitner BJ, Schram JL;

XX DR WPI; 1999-001406/01.

XX PT New detector oligo:nucleotide having base-paired region carrying  
 quenched dyes - where dyes become fluorescent when region is  
 unpaired, useful for detection and amplification of target nucleic  
 acid

XX PS Example 2; Page 12; 20pp; English.

CC Target oligonucleotides AAV82665-68 were designed to hybridize to the  
 detector oligonucleotide of the invention. The detector oligonucleotide  
 comprises a single-stranded target-binding region and an  
 intramolecularly base-paired secondary structure linked to two dyes  
 (donor and acceptor fluorophores). In the secondary structure,  
 fluorescence of the donor is quenched, but when it is linearized or  
 unfolded a change in some fluorescence parameter becomes detectable. A  
 target nucleic acid is detected by hybridizing it to a detector  
 oligonucleotide in which the secondary structure is 5' to the target  
 binding region, primer extension to produce a complementary strand using  
 the secondary structure as template, resulting in linearization or  
 unfolding of it and detecting a change in fluorescence. The detector  
 oligonucleotide are used to detect (by primer extension and  
 hybridization) and amplify (as signal primer) target sequences, e.g. for  
 detecting frameshift mutations.

XX SQ Sequence 48 BP; 15 A; 8 C; 10 G; 15 T; 0 other;

Query Match 64.0%; Score 12.8; DB 20; Length 48;  
 Best Local Similarity 87.5%; Pred. NO. 1.2e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 taccaggtagtctt 18  
 ||| ||| ||| ||| ||| ||| |||  
 Db 41 TACTCAGATGAGTCTT 26

RESULT 12

XX ID AAF62963 standard; DNA; 20 BP.

XX AC AAF62963;

XX DT 08-MAY-2001 (first entry)

XX DE Mouse PEPCK-cytosolic antisense oligonucleotide ISIS 113360.

XX KW Mouse; antiinflammatory; cytostatic; antisense gene therapy;

XX KW phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic;  
 infection; Inflammation; tumour formation; phosphorothioate; ss.

XX OS Mus musculus.

XX PN US6187545-B1.

XX PD 13-FEB-2001.

XX PF 21-JAN-2000; 2000US-0488671.

XX PR 21-JAN-2000; 2000US-0488671.

XX PA (ISIS-) ISIS PHARM INC.

XX PI McKay R, Butler MM, Wyatt J, Cowse LM;

XX DR WPI; 2001-190979/19.

XX PT Antisense compound capable of modulating the expression of phosphoenol  
 pyruvate carboxykinase-cytosolic, useful for preventing or delaying  
 infection, inflammation or tumor formation -

XX PS Example 17; Column 44; 64pp; English.

XX CC The present sequence is one of a number of antisense compounds of up to  
 30 nucleobases in length that are capable of inhibiting the expression of  
 phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The  
 antisense compounds are useful for inhibiting the expression of  
 PEPCK-cytosolic in cells or tissues. They are commonly used as research  
 reagents and in diagnostics, e.g. to elucidate the function of particular  
 genes. They are also useful for distinguishing between functions of  
 various members of a biological pathway and for research use. The  
 antisense compounds are also useful prophylactically, e.g. to prevent or  
 delay infection, inflammation or tumour formation. The present sequence  
 is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a  
 deoxy gap.

XX SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

Query Match 62.0%; Score 12.4; DB 22; Length 20;  
 Best Local Similarity 92.9%; Pred. NO. 1.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 cccaggtagtctt 18  
 || ||| ||| ||| ||| ||| |||  
 Db 15 CCAAGGTGAGTCTT 2

RESULT 13

XX ID AAQ82668 standard; DNA; 22 BP.

XX AC AAQ82668;

XX DT 14-SEP-1995 (first entry)

XX DE Chromosome 11 (locus LDHC) STS primer LDHC-Z.

XX KW sequence sampled mapping; genomic analysis; complex genome mapping;  
 cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.  
 XX OS Synthetic.

PN WO9429486-A.  
 XX  
 PD 22-DEC-1994.  
 XX  
 PF 15-JUN-1994; 94WO-US06810.  
 XX  
 XX 15-JUN-1993; 93US-0078471.  
 PR 07-SEP-1993; 93US-0117952.  
 XX  
 XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
 PA  
 XX Evans GA, Smith MW;  
 PI  
 XX WPI; 1995-036508/05.  
 DR  
 XX

XX Sequencing complex genomes, present as fragments in a cosmid  
 PT library - by sequencing end-specific nucleotides of each clone  
 PT then correlating with spatial relationship of cosmid, esp. for  
 PT mammalian chromosomes.  
 XX

XX Example 4; Page 92; 128pp; English.

XX Sequences were determined from the ends of chromosome 11-specific  
 CC cosmid by automated sequencing without intermediate subcloning.  
 CC A sample of 371 DNA sequence fragments were determined and of  
 CC these, 277 were suitable for STS primer prediction by computer  
 CC analysis (using the "primer" program available from E.Lander, MIT).  
 CC The STSS and cosmid were mapped by in situ hybridisation, somatic  
 CC cell hybrid analysis or both. Using this method, 370 STSS specific  
 CC for human chromosome 11 were generated and most of them were  
 CC regionally mapped. This procedure illustrates a novel method for  
 CC sequencing complex genomes, designated "sequence sampled mapping".  
 CC The sequence sampled mapping method is useful for the completion of  
 CC high density sequence-based maps, and ultimately, for the complete  
 CC sequencing of genomic DNA directly from cosmid clones.  
 CC See AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers.  
 XX

SQ Sequence 22 BP; 8 A; 5 C; 4 G; 5 T; 0 other;

Query Match 62.0%; Score 12.4; DB 16; Length 22;  
 Best Local Similarity 92.9%; Pred. No. 1.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 acccaggtgagtct 17  
 DB 14 ATCCAGGTGAGTCT 1

RESULT 14  
 AAQ86221  
 ID AAQ86221 standard; DNA; 33 BP.  
 XX  
 AC AAQ86221;

XX 12-DEC-1995 (first entry)  
 DT  
 XX GC PCR primer #2.  
 DE  
 XX

KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;  
 KW transcription initiation; non-structural protein; subgenomic fragment;  
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;  
 KW primer; polymerase chain reaction; cystic fibrosis;  
 KW glucocerebrosidase; ss.

OS Synthetic.

XX WO9507994-A.

XX 23-MAR-1995.

PF 15-SEP-1994; 94WO-US10469.

XX

PR 15-SEP-1993; 93US-0122791.  
 PR 18-FEB-1994; 94US-0198450.  
 XX  
 PA (VIAG-) VIAGENE INC.  
 XX  
 PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;  
 PI POLO JM;  
 XX  
 XX WPI; 1995-131362/17.  
 DR  
 XX New alpha virus vectors for gene therapy - of viral infection,  
 PT cancer, auto-immune disease, etc., and as vaccines.  
 PT  
 XX Example 13; Page 154; 260pp; English.

XX The sequences given in AAQ86220-21 are primers which were used in the  
 CC construction of a Sindbis glucocerebrosidase (GC) vector producing  
 CC cell line. These primers amplify a 521 bp fragment for GC screening  
 CC of the transformant cell lines. The cell lines contain alphavirus  
 CC vectors which express multiple heterologous genes. The vectors are  
 CC eukaryotic layered vector initiation systems (ELVIS) derived from  
 CC Sindbis. ELVIS's comprise a 5' sequence capable of initiating  
 CC transcription of an alphavirus, a nucleotide sequence encoding  
 CC alphavirus non-structural proteins, a viral junction region which  
 CC has been inactivated such that viral transcription of the subgenomic  
 CC fragment is prevented, and an alphavirus RNA polymerase recognition  
 CC sequence. Inactivation of the viral junction region prevents  
 CC transcription of the subgenomic fragment making vectors such as this  
 CC suitable for a wide variety of applications, eg. gene therapy for the  
 CC treatment of cystic fibrosis.  
 XX

SQ Sequence 33 BP; 10 A; 5 C; 11 G; 7 T; 0 other;

Query Match 62.0%; Score 12.4; DB 16; Length 33;  
 Best Local Similarity 92.9%; Pred. No. 1.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agtaccaggtgag 14  
 DB 6 agtagccaggtgag 19

RESULT 15  
 AAQ86223  
 ID AAQ86223 standard; DNA; 33 BP.  
 XX  
 AC AAQ86223;

XX 12-DEC-1995 (first entry)  
 DT  
 XX GC PCR (R) primer #2.  
 DE  
 XX

KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;  
 KW transcription initiation; non-structural protein; subgenomic fragment;  
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;  
 KW primer; polymerase chain reaction; cystic fibrosis;  
 KW glucocerebrosidase; ss.

OS Synthetic.

XX WO9507994-A.

XX 23-MAR-1995.

PF 15-SEP-1994; 94WO-US10469.

XX 15-SEP-1993; 93US-0122791.

XX 18-FEB-1994; 94US-0198450.

XX (VIAG-) VIAGENE INC.

PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;

PI Polo JM;  
XX  
DR WPI; 1995-131362/17.  
XX  
XX  
PT New alpha virus vectors for gene therapy - of viral infection,  
PT cancer, auto-immune disease, etc., and as vaccines.  
XX  
XX  
PS Example 17; Page 166; 260pp; English.  
XX  
XX The sequences given in AA086222-23 are primers which were used in the  
CC construction of a Sindbis glucocerebrosidase (GC) vector producing  
CC cell line. These primers amplify a 521 bp fragment for GC screening  
CC of the transformant cell lines. The cell lines contain alphavirus  
CC vectors which express multiple heterologous genes. The vectors are  
CC eukaryotic layered vector initiation systems (ELVIS) derived from  
CC Sindbis. ELVIS's comprise a 5' sequence capable of initiating  
CC transcription of an alphavirus, a nucleotide sequence encoding  
CC alphavirus non-structural proteins, a viral junction region which  
CC has been inactivated such that viral transcription of the subgenomic  
CC fragment is prevented, and an alphavirus RNA polymerase recognition  
CC sequence. Inactivation of the viral junction region prevents  
CC transcription of the subgenomic fragment making vectors such as this  
CC suitable for a wide variety of applications, eg. gene therapy for the  
CC treatment of cystic fibrosis.  
XX  
SQ Sequence 33 BP; 10 A; 5 C; 11 G; 7 T; 0 other;  
  
Query Match 62.0%; Score 12.4; DB 16; Length 33;  
Best Local Similarity 92.9%; Pred. NO. 1.8e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 agtaccagggtgag 14  
   |||||  
Db 6 agtagccagggtgag 19

Search completed: October 2, 2001, 16:18:40  
Job time: 15484 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:48 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-10

Perfect score: 20

Sequence: 1 ggtaagcagctgccattatt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2.6/ptodata/1/ina/PTUS\_COMB.seq:\*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-377-310-10
2	15	75.0	15	3	US-09-377-310-30
3	13.8	69.0	30	2	US-08-471-371-6
4	13.6	68.0	30	2	US-08-833-377-5
5	13.4	67.0	18	1	US-08-378-761A-45
6	13.4	67.0	18	1	US-08-485-286-45
7	13.2	66.0	30	1	US-07-985-691-6
8	12.6	63.0	29	3	US-09-106-216-52
9	12.6	63.0	44	4	US-09-042-353-374
10	12.6	63.0	49	3	US-09-106-216-53
11	12.4	62.0	39	2	US-08-484-397A-24
12	12.2	61.0	25	1	US-08-482-115B-26
13	12.2	61.0	25	1	US-08-752-929-22
14	12.2	61.0	25	2	US-08-472-802C-27
15	12.2	61.0	41	5	US-09-042-353-374
16	12.2	61.0	45	3	US-08-617-454-9
17	12.2	61.0	49	2	US-09-157-206-5
18	12.2	61.0	49	4	US-09-447-863-5
19	12.2	61.0	49	5	US-09-447-863-5
20	12	60.0	29	3	US-08-826-964-4
21	12	60.0	39	2	US-08-951-822-13
22	12	60.0	39	4	US-09-173-043-28
23	12	60.0	42	2	US-08-436-664-3
24	12	60.0	42	2	US-08-436-664-4
25	12	60.0	42	3	US-09-135-642-3
26	12	60.0	42	3	US-09-135-642-4
27	12	60.0	42	3	US-08-394-232A-3

ALIGNMENTS

RESULT 1

US-09-377-310-10  
; Sequence 10, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-10

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtaagcagctgccattatt 20  
Db 1 ||||| ||||| ||||| ||||| |||||

RESULT 2

US-09-377-310-30  
; Sequence 30, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

Sequence 4, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 18, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 9, Appli  
Sequence 25, Appl  
Sequence 28, Appl  
Sequence 25, Appl  
Sequence 28, Appl  
Sequence 28, Appl

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; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-30

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Query Match      75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels
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Qy 3 taagcagctgccatt 17  
|||  
Db 1 taagcagctgccatt 15

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RESULT      3
US-08-471-371-6
; Sequence 6, Application US/08471371
; Patent No. 5981215
; GENERAL INFORMATION:
; APPLICANT: Meissner, Paul S.
; APPLICANT: Coleman, Timothy A.
; TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: N.J.
; COUNTRY: U.S.A
; ZIP: 07068

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/RMS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,371
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32580-455
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PRIMER"
US-08-471-371-6

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Query Match 69.0%; Score 13.8; DB 2; Length 30;  
Best Local Similarity 88.2%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels

Qy 4 aagcagctgccattatt 20  
|| ||||| |||||  
Db 4 AACCAGCTGCTATTATT 20

RESULT 4  
US-08-833-377-5  
; Sequence 5, Application US/08833377  
; Patent No. 5968506  
; GENERAL INFORMATION:  
; APPLICANT: Weinrich, Scott L.

APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtstelnier, Serge P.  
APPLICANT: Vasserot, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..30  
OTHER INFORMATION: /note= "Oligo 13"  
1-833-377-5

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Query Match      68.0%; Score 13.6; DB 2; Length 30;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 16: Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 ggtaagcagctgccattatt 20  
||| ||||| ||||| ||  
Db 6 GGCCAGCAGCTGACATTTT 25

```

RESULT      5
US-08-378-761A-45/c
; Sequence 45, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEV, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACT
; TITLE OF INVENTION: PRECURSOR FOR
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81

```



; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANDREA T. BORUCKI  
; STREET: 9330 ZIONSVILLE ROAD  
; CITY: INDIANAPOLIS  
; STATE: IN  
; COUNTRY: US  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,761A  
; FILING DATE: 26-JAN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BORUCKI, ANDREA T  
; REGISTRATION NUMBER: 33651  
; REFERENCE/DOCKET NUMBER: 38272B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 337-4846  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-378-761A-45

Query Match 67.0%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 2.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 taagcagctgccatt 17  
| | | | | | | | | | | | | | | | | | | |  
Db 17 TAAGCAGCTGCAATT 3

RESULT 6  
US-08-485-286-45/c  
; Sequence 45, Application US/08485286  
; Patent No. 5646026  
; Patent No. 5646026 5646119  
; GENERAL INFORMATION:  
; APPLICANT: WALSH, TERENCE A  
; APPLICANT: HEY, TIMOTHY D  
; APPLICANT: MORGAN, ALICE ER  
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
; TITLE OF INVENTION: USING  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANDREA T. BORUCKI  
; STREET: 9330 ZIONSVILLE ROAD  
; CITY: INDIANAPOLIS  
; STATE: IN  
; COUNTRY: US  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,286  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/378761  
; FILING DATE: 26-JAN-1995  
; ATTORNEY/AGENT INFORMATION:

; NAME: BORUCKI, ANDREA T  
; REGISTRATION NUMBER: 33651  
; REFERENCE/DOCKET NUMBER: 38272B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 337-4846  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-485-286-45

Query Match 67.0%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 2.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 taagcagctgccatt 17  
| | | | | | | | | | | | | | | | | | | |  
Db 17 TAAGCAGCTGCAATT 3

RESULT 7  
US-07-985-691-6/c  
; Sequence 6, Application US/07985691  
; Patent No. 5405946  
; GENERAL INFORMATION:  
; APPLICANT: Griffin, John H  
; APPLICANT: Bouma, Bonno N  
; APPLICANT: Bertina, Rogier  
; TITLE OF INVENTION: RECOMBINANT PROTEIN S VARIANTS DEFICIENT  
; TITLE OF INVENTION: IN C4BP BINDING ACTIVITY, COMPOSITIONS AND THERAPEUTIC  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5405946th Torrey Pines Road, TPC 8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/985,691  
; FILING DATE: 19921202  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSR0042P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-07-985-691-6

Query Match 66.0%; Score 13.2; DB 1; Length 30;  
Best Local Similarity 83.3%; Pred. No. 3.3e+02;



; FILING DATE: 01-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 014643-009040US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 374:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-042-353-374

Query Match 63.0%; Score 12.6; DB 4; Length 44;  
Best Local Similarity 78.9%; Pred. No. 7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ggtaagcagctgcccattat 19  
Db 26 GCTAACCAGCTGCTAATAT 8

## RESULT 10

US-09-106-216-53/c  
; Sequence 53, Application US/09106216  
; Patent No. 6153386  
; GENERAL INFORMATION:  
; APPLICANT: Lalouel, Jean-Marie  
; APPLICANT: Jeunemaitre, Xavier  
; APPLICANT: Lofton, Richard P.  
; APPLICANT: Soubrier, Florent  
; APPLICANT: Kotelevtsev, Yuri  
; APPLICANT: Corvol, Pierre  
; TITLE OF INVENTION: Method to Determine Predisposition to  
; TITLE OF INVENTION: Hypertension  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
; STREET: 555 Thirteenth Street N.W., Suite 701-E  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/106,216  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/  
; FILING DATE: 08-JUN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/319,545  
; FILING DATE: 07-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952,545  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 2323-124  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031

; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 49 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer"  
US-09-106-216-53

Query Match 63.0%; Score 12.6; DB 3; Length 49;  
Best Local Similarity 78.9%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gtaagcagctgcccattatt 20  
Db 46 GGAAGAGCTCCCGTTGTT 28

## RESULT 11

US-08-484-397A-24/c  
; Sequence 24, Application US/08484397A  
; Patent No. 5869055  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Shao-Chieh  
; APPLICANT: Lichenstein, Henri S.  
; APPLICANT: Wright, Samuel D.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,397A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Curry, Daniel R.  
; REGISTRATION NUMBER: 32,727  
; REFERENCE/DOCKET NUMBER: A-324A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/447-1000  
; TELEFAX: 805/447-1090  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-484-397A-24

Query Match 62.0%; Score 12.4; DB 2; Length 39;  
Best Local Similarity 92.9%; Pred. No. 8.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 agcagctgcccatta 18  
Db 24 AGCAGCTGCCCTTTA 11

## RESULT 12

US-08-482-115B-26  
 ; Sequence 26, Application US/08482115B  
 ; Patent No. 5776679  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Villeponteau, Bryant  
 ; APPLICANT: Feng, Junli  
 ; APPLICANT: Funk, Walter  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: Assays for the RNA Component of Human  
 ; TITLE OF INVENTION: Telomerase  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/482,115B  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/272,102  
 ; FILING DATE: 07-JUL-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/330,123  
 ; FILING DATE: 27-OCT-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Storella, John R.  
 ; REGISTRATION NUMBER: 32,944  
 ; REFERENCE/DOCKET NUMBER: 015389-000830US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 26:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-482-115B-26

Query Match 61.0%; Score 12.2; DB 1; Length 25;  
 Best Local Similarity 82.4%; Pred. No. le+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ggaagcagctgccatt 17  
 || ||||| |||||  
 DB 9 GGCCAGCAGCTGACATT 25

RESULT 13  
 US-08-752-929-22  
 ; Sequence 22, Application US/08752929  
 ; Patent No. 5798259  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YAZAWA, Kazunaga  
 ; APPLICANT: YAMADA, Akiko  
 ; APPLICANT: KATO, Seishi  
 ; APPLICANT: KONDO, Kiyoshi  
 ; TITLE OF INVENTION: Gene Coding for Eicosapentaenoic Acid Synthesizing  
 ; TITLE OF INVENTION: Enzymes and Process for Production of Eicosapentaenoic  
 ; TITLE OF INVENTION: Acid  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/752,929  
 ; FILING DATE: 20-NOV-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/375,709  
 ; FILING DATE: 20-JAN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/178,251  
 ; FILING DATE: 14-MAY-1993  
 ; APPLICATION NUMBER: JP 4-147945  
 ; FILING DATE: 15-MAY-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WEGNER, Harold C.  
 ; REGISTRATION NUMBER: 25,258  
 ; REFERENCE/DOCKET NUMBER: 53466/150/AAOK  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 22:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-752-929-22

Query Match 61.0%; Score 12.2; DB 1; Length 25;  
 Best Local Similarity 82.4%; Pred. No. le+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 taagcagctgccattat 19  
 | | | | | | | | | |  
 DB 5 TCATCAGGTGCCATTAT 21

RESULT 14  
 US-08-472-802C-27  
 ; Sequence 27, Application US/08472802C  
 ; Patent No. 5958680  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Villeponteau, Bryant  
 ; APPLICANT: Feng, Junli  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: Mammalian Telomerase  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,802C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-472-802C-27

Query Match 61.0%; Score 12.2; DB 2; Length 25;  
Best Local Similarity 82.4%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ggtaagcagctgccatt 17  
||| ||||| |||||  
Db 9 GCCCAGCAGCTGACATT 25

## RESULT 15

PCT-US96-09455A-186/c  
Sequence 186, Application PC/TUS9609455A  
GENERAL INFORMATION:  
APPLICANT: PARMA, et al.  
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID  
LIGANDS TO LECTINS  
NUMBER OF SEQUENCES: 390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09455A  
FILING DATE: 05 JUNE 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,724  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/472,256  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/472,255  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,829  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX40C/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 186:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
PCT-US96-09455A-186

Query Match 61.0%; Score 12.2; DB 5; Length 41;  
Best Local Similarity 82.4%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 gtaagcagctgccatta 18  
||| ||||| |||||  
Db 41 GTAAGCCGAGGCCATTA 25

Search completed: October 2, 2001, 16:03:49  
Job time: 14593 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:07 ; Search time 2173.58 Seconds  
(without alignments)  
14.467 Million cell updates/sec

Title: US-09-757-100B-33  
Perfect score: 15  
Sequence: 1 tggctattcttcagt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	12.4	82.7	20	6	US-09-198-452A-3994
2	11.8	78.7	21	7	US-09-849-243-7
3	11.8	78.7	24	5	US-09-815-980-1
4	11.4	76.0	31	5	US-09-536-784-272
5	11.4	76.0	31	6	US-09-765-272-272
6	11.4	76.0	31	7	US-09-717-438-14
7	11.4	76.0	31	7	US-09-724-750-14025
8	11.4	76.0	31	7	US-09-724-750-24046
9	11.4	76.0	31	7	US-09-717-438-13
10	10.8	72.0	17	7	US-09-818-875-1707
11	10.8	72.0	17	7	US-09-818-875-1708
12	10.8	72.0	20	6	US-09-743-237-16
13	10.8	72.0	20	6	US-09-198-452A-1913
14	10.8	72.0	21	7	US-09-520-313-140
15	10.8	72.0	23	7	US-09-379-888B-8
16	10.8	72.0	31	5	US-09-700-492-3
17	10.4	69.3	17	5	US-09-708-690-9178
18	10.4	69.3	17	5	US-09-708-690-9179
19	10.4	69.3	17	6	US-09-866-108-1237
20	10.4	69.3	17	6	US-09-866-108-1238
21	10.4	69.3	17	6	US-09-866-108-1239
22	10.4	69.3	17	6	US-09-866-108-1240
23	10.4	69.3	17	6	US-09-866-108-1241
24	10.4	69.3	17	6	US-09-866-108-1242
25	10.4	69.3	17	6	US-09-866-108-2547

ALIGNMENTS

RESULT 1  
US-09-198-452A-3994  
; Sequence 3994, Application US/09198452A  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 3994  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-3994

Query Match 82.7% Score 12.4; DB 6; Length 20;  
Best Local Similarity 92.9%; Pred. No. 1.1e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ggcttattcttcagt 15  
Db 1 ggcttattcttcagt 14

RESULT 2  
US-09-849-243-7/c  
; Sequence 7, Application US/09849243  
; GENERAL INFORMATION:  
; APPLICANT: Kirschbaum, Bernd  
; Berglund, Erick  
; Meisterernst, Michael  
; Polites, Greg  
; TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION COMPLEXES FROM TRANSGENIC NON-HUMAN ANIMALS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HELLER, EHRMAN, WHITE & MCAULIFFE  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/849,243  
;; FILING DATE: 07-May-2001  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granados, Patricia D.  
;; REGISTRATION NUMBER: 33,683  
;; REFERENCE/DOCKET NUMBER: 38005-0148  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)912-2000  
;; TELEFAX: (202)912-2020  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: exon  
;; LOCATION: 1..21  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-849-243-7

Query Match 78.7%; Score 11.8; DB 7; Length 21;  
Best Local Similarity 86.7%; Pred. No. 2.5e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 tggcttatcttcag 15  
||||| || |||||  
Db 19 TGGCCTAACTTCAGT 5

RESULT 3  
US-09-815-980-1/c  
; Sequence 1, Application US/09815980  
; GENERAL INFORMATION:  
; APPLICANT: Leiden, Jeffrey M.  
; TITLE OF INVENTION: AN INDUCIBLE EUKARYOTIC EXPRESSION  
; TITLE OF INVENTION: SYSTEM THAT REGULATES PROTEIN TRANSLATION  
; FILE REFERENCE: HUI-042  
; CURRENT APPLICATION NUMBER: US/09/815,980  
; CURRENT FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 60/191,568  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-815-980-1

Query Match 78.7%; Score 11.8; DB 5; Length 24;  
Best Local Similarity 86.7%; Pred. No. 2.6e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 tggcttatcttcag 15  
||||| || |||||  
Db 18 TGGCCTAACTTCAGT 4

RESULT 4  
US-09-536-784-272  
; Sequence 272, Application US/09536784  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.

;; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
;; NUMBER OF SEQUENCES: 452  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Human Genome Sciences, Inc.  
;; STREET: 9410 Key West Avenue  
;; CITY: Rockville  
;; STATE: Maryland  
;; COUNTRY: USA  
;; ZIP: 20850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
;; COMPUTER: HP Vectra 486/33  
;; OPERATING SYSTEM: MSDOS version 6.2  
;; SOFTWARE: ASCII Text  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/536,784  
;; FILING DATE: 30-Oct-1997  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/961,083  
;; FILING DATE: OCT-30-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Michelle S. Marks  
;; REGISTRATION NUMBER: 41,971  
;; REFERENCE/DOCKET NUMBER: PB340P3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (301) 309-8504  
;; TELEFAX: (301) 309-8512  
;; INFORMATION FOR SEQ ID NO: 272:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 31 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 272:  
US-09-536-784-272

Query Match 76.0%; Score 11.4; DB 5; Length 31;  
Best Local Similarity 92.3%; Pred. No. 4.6e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 gcttatcttcag 15  
||||| |||||  
Db 7 GCTTATCTGCAGT 19

RESULT 5  
US-09-765-272-272  
; Sequence 272, Application US/09765272  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Human Genome Sciences, Inc.  
;; STREET: 9410 Key West Avenue  
;; CITY: Rockville  
;; STATE: Maryland  
;; COUNTRY: USA  
;; ZIP: 20850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
;; COMPUTER: HP Vectra 486/33  
;; OPERATING SYSTEM: MSDOS version 6.2  
;; SOFTWARE: ASCII Text  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/765,272  
;; FILING DATE: 22-Jan-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/961,083  
;; FILING DATE: <Unknown>



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; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-765-272-272

Query Match 76.0%; Score 11.4; DB 6; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gcttatcttcagt 15
Db 7 GCTTATCTGCAGT 19

RESULT 6
US-09-717-438-14
; Sequence 14, Application US/09717438
; GENERAL INFORMATION:
; APPLICANT: Cramer, Willem P.C.
; TITLE OF INVENTION: Methods for Generating Polynucleotides
; Having Desired Characteristics by Iterative Selection and
; Recombination
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/717,438
; FILING DATE: 18-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,859
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/537,874
; FILING DATE: 30-OCT-1995
; APPLICATION NUMBER: WO PCT/US95/02126
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: US 08/198,431
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018097-014612US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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```
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-717-438-14

Query Match 73.3%; Score 11; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 cttatcttcag 14
Db 2 CTTATCTTCAG 12

RESULT 7
US-09-724-750-14025
; Sequence 14025, Application US/09724750
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Polynucleotide, Materials Incorporating
; FILE REFERENCE: 11000.1049AU
; CURRENT APPLICATION NUMBER: US/09/724,750
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/171,431
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 25199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14025
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-724-750-14025

Query Match 73.3%; Score 11; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ggcttatcttc 12
Db 27 ggcttatcttc 37

RESULT 8
US-09-724-750-24046
; Sequence 24046, Application US/09724750
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Polynucleotide, Materials Incorporating
; FILE REFERENCE: 11000.1049AU
; CURRENT APPLICATION NUMBER: US/09/724,750
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/171,431
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 25199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24046
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-724-750-24046

Query Match 73.3%; Score 11; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ggcttatcttc 12
Db 23 ggcttatcttc 33
```

RESULT 9  
US-09-717-438-13/c  
; Sequence 13, Application US/09717438  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P.C.  
; Cramer, Andreas M.  
; TITLE OF INVENTION: Methods for Generating Polynucleotides  
; Having Desired Characteristics by Iterative Selection and  
; Recombination  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/717,438  
; FILING DATE: 18-Nov-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,859  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/537,874  
; FILING DATE: 30-OCT-1995  
; APPLICATION NUMBER: WO PCT/US95/02126  
; FILING DATE: 17-FEB-1995  
; APPLICATION NUMBER: US 08/198,431  
; FILING DATE: 17-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018097-01461205  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-717-438-13

Query Match 73.3%; Score 11; DB 7; Length 41;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cttatcttcag 14  
| | | | | | | | | |  
DB 22 CTTATCTTCAG 12

RESULT 10  
US-09-818-875-1707  
; Sequence 1707, Application US/09818875  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gampfer, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; Stranded Oligonucleotides

; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 1707  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-1707

Query Match 72.0%; Score 10.8; DB 7; Length 17;  
Best Local Similarity 85.7%; Pred. No. 9.2e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tggcttatcttcag 14  
| | | | | | | | | |  
DB 4 tagtttatcttcag 17

RESULT 11  
US-09-818-875-1708/c  
; Sequence 1708, Application US/09818875  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gampfer, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; Stranded Oligonucleotides

; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 1708  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-1708

Query Match 72.0%; Score 10.8; DB 7; Length 17;  
Best Local Similarity 85.7%; Pred. No. 9.2e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tggcttatcttcag 14  
| | | | | | | | | |  
DB 14 TAGTTTATCTTCAG 1

RESULT 12  
US-09-743-237-16/c  
; Sequence 16, Application US/09743237  
; GENERAL INFORMATION:  
; APPLICANT: SUGIHARA, TAKASHI  
; APPLICANT: WADHWA, RENU

; APPLICANT: KAUL, SUNIL C.  
; APPLICANT: MITSUI, YUJI  
; TITLE OF INVENTION: TESTIS-SPECIFIC DIFFERENTIATION-REGULATORY FACTOR  
; FILE REFERENCE: 084335/0127  
; CURRENT APPLICATION NUMBER: US/09/743,237  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/JP99/03859  
; PRIOR FILING DATE: 1999-07-16  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-743-237-16

Query Match 72.0%; Score 10.8; DB 6; Length 20;  
Best Local Similarity 85.7%; Pred. No. 9.4e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ggcttattcttcagt 15  
||||| ||||| |||  
Db 19 GGCTTGCTCTTGAGT 6

RESULT 13  
US-09-198-452A-1913/c  
; Sequence 1913, Application US/09198452A  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 1913  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-1913

Query Match 72.0%; Score 10.8; DB 6; Length 20;  
Best Local Similarity 85.7%; Pred. No. 9.4e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttattcttcag 14  
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Db 15 TGGATTAACTTCAG 2

RESULT 14  
US-09-920-313-140/c  
; Sequence 140, Application US/09920313  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; TITLE OF INVENTION: Nucleic Acids for the Prevention and  
; TITLE OF INVENTION: Treatment of Gastric Ulcers  
; FILE REFERENCE: C1037/7019 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/920,313  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: US 60/222,248  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 140  
; LENGTH: 21

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-920-313-140

Query Match 72.0%; Score 10.8; DB 7; Length 21;  
Best Local Similarity 85.7%; Pred. No. 9.5e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttattcttcag 14  
||||| ||||| |||||  
Db 15 TGGCTTCTGTTTCAG 2

RESULT 15  
US-09-379-888B-8  
; Sequence 8, Application US/09379888B  
; GENERAL INFORMATION:  
; APPLICANT: Huan, Bingfang  
; APPLICANT: Albagli, David  
; APPLICANT: Wood, Michael L.  
; APPLICANT: Van Atta, Reuel B.  
; APPLICANT: Cheng, Peter C.  
; TITLE OF INVENTION: Assays Using Crosslinkable Immobilized Nucleic Acids  
; FILE REFERENCE: 14251-0006 CIP  
; CURRENT APPLICATION NUMBER: US/09/379,888B  
; CURRENT FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: nucleic acid probe  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: fluorescein attached at 5' end  
; NAME/KEY: source  
; LOCATION: (1)..(23)  
; OTHER INFORMATION: chemically synthesized or biologically prepared nucleic acid  
; NAME/KEY: misc\_feature  
; LOCATION: (22)..(23)  
; OTHER INFORMATION: 3-O-(7-coumarinyl)-glycerol between position 22 and 23  
US-09-379-888B-8

Query Match 72.0%; Score 10.8; DB 7; Length 23;  
Best Local Similarity 85.7%; Pred. No. 9.6e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttattcttcag 14  
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Db 5 ttgcttattcttcag 18

Search completed: October 2, 2001, 16:55:07  
Job time: 17670 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:21 ; Search time 17695.9 Seconds  
(without alignments)  
12.526 Million cell updates/sec

Title: US-09-757-100B-33

Perfect score: 15

Sequence: 1 tggcttatcttcagt 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	15	100.0	15	17	US-09-377-310-33
3	15	100.0	15	29	US-09-757-100B-33
4	15	100.0	20	1	PCT-US00-18999-13
5	15	100.0	20	14	US-09-050-392-15
6	15	100.0	20	17	US-09-377-310-13
7	15	100.0	20	29	US-09-757-100B-13
8	13.4	89.3	25	55	US-60-233-166-354400
9	12.4	82.7	18	18	US-09-422-978-3990
10	12.4	82.7	27	6	US-08-292-683-11
11	12.4	82.7	27	9	US-08-516-859-11
12	12.4	82.7	27	19	US-09-528-706-11
13	12.4	82.7	27	22	US-09-586-472-11
14	12	80.0	18	53	US-60-216-745-7663
15	12	80.0	19	24	US-09-638-509C-18
16	12	80.0	21	25	US-09-657-472-179
17	12	80.0	25	55	US-60-234-017-312510
18	12	80.0	25	55	US-60-234-017-469082
19	12	80.0	37	31	US-09-826-509-241
20	12	80.0	37	31	US-09-826-509-242
21	11.8	78.7	22	12	US-08-896-155-16
22	11.8	78.7	22	31	US-09-845-079-16
23	11.8	78.7	22	31	US-09-852-156-16
24	11.8	78.7	25	26	US-09-660-220-39947
25	11.8	78.7	25	26	US-09-660-220-52789
26	11.8	78.7	25	26	US-09-660-220-52790
27	11.8	78.7	25	26	US-09-660-220-88553
28	11.8	78.7	25	55	US-60-232-638-93376
29	11.8	78.7	25	55	US-60-232-638-93376
30	11.8	78.7	25	55	US-60-232-638-138151
31	11.8	78.7	25	55	US-60-232-638-138162
32	11.8	78.7	25	55	US-60-233-166-157273
33	11.8	78.7	25	55	US-60-233-166-288539
34	11.8	78.7	25	55	US-60-233-166-288539
35	11.8	78.7	25	55	US-60-234-017-66106
36	11.8	78.7	25	55	US-60-234-017-298566
37	11.8	78.7	25	55	US-60-234-017-411280
38	11.8	78.7	25	55	US-60-234-017-476987
39	11.8	78.7	25	55	US-60-234-017-476988
40	11.8	78.7	25	55	US-60-234-017-490690
41	11.8	78.7	30	6	US-08-087-784-9
42	11.8	78.7	30	6	US-08-268-880-9
43	11.8	78.7	30	8	US-08-407-128-10
44	11.8	78.7	30	8	US-08-409-770-10
45	11.8	78.7	30	8	US-08-423-292-9

US 09-757-100B-33  
: Sequence 33. Application IIS/09757100B

```
; APPLICANT: Aotsuka, Satoshi
; APPLICANT: Hayashi, Takahisa
; APPLICANT: Ihara, Yuri
; TITLE OF INVENTION: Cellulose Synthase Gene
; FILE REFERENCE: 20111-0017
; CURRENT APPLICATION NUMBER: US/09/050,392A
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: JP 9-83133
; EARLIER FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-050-392-15

Query Match          100.0%; Score 15; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggcttatcttcagt 15
Db 16 TGGCTTATCTTCAGT 2

RESULT 6
US-09-377-310-13
; Sequence 13, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-13

Query Match          100.0%; Score 15; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggcttatcttcagt 15
Db 3 tggcttatcttcagt 17

RESULT 7
US-09-757-100b-13
; Sequence 13, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
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; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100b-13

Query Match          100.0%; Score 15; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggcttatcttcagt 15
Db 3 tggcttatcttcagt 17

RESULT 8
US-60-233-166-354400
; Sequence 354400, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354400
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U65486
US-60-233-166-354400

Query Match          89.3%; Score 13.4; DB 55; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tggcttatcttcagt 15
Db 4 tggcttatcttcagt 18

RESULT 9
US-09-422-978-3990/c
; Sequence 3990, Application US/09422978
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3990
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```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-12619 for SEQ 56,
US-09-422-978-3990

Query Match      82.7%; Score 12.4; DB 18; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.le+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ggcttatcttcagt 15
    ||||| |||||
Db 18 GGCATTATTTTCAGT 5

RESULT 10
US-08-292-683-11/c
; Sequence 11, Application US/08292683
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding RIZ
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,683
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1004
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-683-11

Query Match      82.7%; Score 12.4; DB 6; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.le+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tggcttatcttcag 14
    ||||| |||||
Db 27 TGGCTTTTCTTCAG 14

RESULT 11
US-08-516-859-11/c
; Sequence 11, Application US/08516859
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
```

```
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-516-859-11

Query Match      82.7%; Score 12.4; DB 9; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.le+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tggcttatcttcag 14
    ||||| |||||
Db 27 TGGCTTTTCTTCAG 14

RESULT 12
US-09-528-706-11/c
; Sequence 11, Application US/09528706
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
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; FILING DATE: 18-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1776  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-528-706-11

Query Match 82.7%; Score 12.4; DB 19; Length 27;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tggcttattctcag 14  
||||| |||||||  
DB 27 TGGCTTTCTTCAG 14

## RESULT 13

US-09-586-472-11/c  
; Sequence 11, Application US/09586472

## ; GENERAL INFORMATION:

; APPLICANT: Huang, Shi  
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
; Zinc Finger Proteins

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92122

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/586,472

; FILING DATE: 01-Jun-2000

; CLASSIFICATION: <Unknown>

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/528,706

; FILING DATE: 17-MAR-2000

; APPLICATION NUMBER: US 08/516,859

; FILING DATE: 18-AUG-1995

; APPLICATION NUMBER: US 08/399,411

; FILING DATE: 06-MAR-1995

; APPLICATION NUMBER: US 08/292,683

; FILING DATE: 18-AUG-1994

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LJ 4130

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

## ; INFORMATION FOR SEQ ID NO: 11:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 27 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

## US-09-586-472-11

Query Match 82.7%; Score 12.4; DB 22; Length 27;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tggcttattctcag 14  
||||| |||||||  
DB 27 TGGCTTTCTTCAG 14

## RESULT 14

US-60-216-745-7663

; Sequence 7663, Application US/60216745

## ; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; APPLICANT: Abderrahim, Hadi

; APPLICANT: Dufaire-Gare, Isabelle

; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY.

; FILE REFERENCE: 84.US1.PRO

; CURRENT APPLICATION NUMBER: US/60/216,745

; CURRENT FILING DATE: 2000-06-30

; NUMBER OF SEQ ID NOS: 13665

; SOFTWARE: Patent.pm

; SEQ ID NO 7663

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer\_bind

; LOCATION: 1..18

; OTHER INFORMATION: upstream amplification primer 99-46755 for SEQ 3132,  
US-60-216-745-7663

## Query Match

80.0%; Score 12; DB 53; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ctattcttcagt 15  
||||| |||||||  
DB 3 ctattcttcagt 14

## RESULT 15

US-09-638-509C-18/c

; Sequence 18, Application US/09638509C

## ; GENERAL INFORMATION:

; APPLICANT: Tang, Jianming

; APPLICANT: Kaslow, Richard A.

; TITLE OF INVENTION: Methods of Surveying For CC (Beta) Chemokine

; TITLE OF INVENTION: Receptor Variants and Their Association With HIV-1

; TITLE OF INVENTION: Transmission and/or Disease Progression

; FILE REFERENCE: D6217

; CURRENT APPLICATION NUMBER: US/09/638,509C

; CURRENT FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/148,530

; PRIOR FILING DATE: 1999-08-12

; NUMBER OF SEQ ID NOS: 35

; SEQ ID NO 18

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: primer\_bind

; OTHER INFORMATION: CCR5-PM6G, primer used for typing major

; OTHER INFORMATION: polymorphism in CCR2b, CCR5 and the CCR5 downstream

; OTHER INFORMATION: promoter region

; US-09-638-509C-18

Query Match 80.0%; Score 12; DB 24; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ggcttatcttca 13  
|||  
Db 15 GGCTTATCTTCA 4

Search completed: October 2, 2001, 21:50:22  
Job time: 24535 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:07 ; Search time 2173.58 Seconds  
(without alignments)  
14.467 Million cell updates/sec

Title: US-09-757-100B-31

Perfect score: 15

Sequence: 1 taccagggtgagtct 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*

- 1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 8: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.4	82.7	33	7	US-09-672-217-122
2	12.4	82.7	33	7	US-09-672-217-223
3	11.4	76.0	25	6	US-09-857-581-65
4	11.4	76.0	31	6	US-09-801-274-1705
5	10.8	72.0	27	7	US-09-794-384A-10
6	10.4	69.3	15	5	US-09-406-643-4
7	10.4	69.3	15	5	US-09-406-643-293
8	10.4	69.3	15	5	US-09-406-643-294
9	10.4	69.3	17	6	US-09-866-108-7712
10	10.4	69.3	17	6	US-09-866-108-7713
11	10.4	69.3	17	6	US-09-866-108-7714
12	10.4	69.3	17	6	US-09-866-108-7715
13	10.4	69.3	17	6	US-09-866-108-7716
14	10.4	69.3	17	6	US-09-866-108-7717
15	10.4	69.3	19	5	US-09-927-796-165
16	10.4	69.3	19	5	US-09-927-796-168
17	10.4	69.3	20	1	PCT-US01-25860-20
18	10.4	69.3	25	6	US-09-866-108-12604
19	10.4	69.3	25	6	US-09-866-108-12605
20	10.4	69.3	25	6	US-09-866-108-12606
21	10.4	69.3	25	6	US-09-866-108-12607
22	10.4	69.3	25	6	US-09-866-108-12608
23	10.4	69.3	25	6	US-09-866-108-12609
24	10.4	69.3	25	6	US-09-866-108-12610
25	10.4	69.3	25	6	US-09-866-108-12611

ALIGNMENTS

RESULT 1

US-09-672-217-122

; Sequence 122, Application US/09672217

; GENERAL INFORMATION:

; APPLICANT: FELL, JACK

; APPLICANT: DIAZ, MARA

; APPLICANT: MCCABE, MEADE

; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI

; FILE REFERENCE: 086222/0143

; CURRENT APPLICATION NUMBER: US/09/672,217

; CURRENT FILING DATE: 2000-09-29

; PRIOR FILING DATE: 1999-09-29

; NUMBER OF SEQ ID NOS: 301

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 122

; LENGTH: 33

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe

US-09-672-217-122

Query Match 82.7%; Score 12.4; DB 7; Length 33;  
Best Local Similarity 92.9%; Pred. No. 1.1e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15

|||||||

Db 17 acccaggtgagtct 30

RESULT 2

US-09-672-217-223

; Sequence 223, Application US/09672217

; GENERAL INFORMATION:

; APPLICANT: FELL, JACK

; APPLICANT: DIAZ, MARA

; APPLICANT: MCCABE, MEADE

; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI

; FILE REFERENCE: 086222/0143

; CURRENT APPLICATION NUMBER: US/09/672,217

; CURRENT FILING DATE: 2000-09-29

; PRIOR FILING DATE: 1999-09-29

; NUMBER OF SEQ ID NOS: 301

; SOFTWARE: PatentIn Ver. 2.1

Sequence 12612, A  
Sequence 12613, A  
Sequence 12614, A  
Sequence 12615, A  
Sequence 12616, A  
Sequence 12617, A  
Sequence 1624, Ap  
Sequence 5614, Ap  
Sequence 43408, A  
Sequence 16237, A  
Sequence 30106, A  
Sequence 13, Appl  
Sequence 10, Appl  
Sequence 51, Appl  
Sequence 49, Appl  
Sequence 10744, A  
Sequence 29, Appl  
Sequence 25, Appl  
Sequence 1321, Ap  
Sequence 1322, Ap

; SEQ ID NO 223  
; LENGTH: 33  
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe  
US-09-672-217-223

Query Match 82.7%; Score 12.4; DB 7; Length 33;  
Best Local Similarity 92.9%; Pred. No. 1.1e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15  
|||||

Db 17 acccaggtgagtct 30  
|||||

RESULT 3

US-09-857-581-65/c

; Sequence 65, Application US/09857581

; GENERAL INFORMATION:

; APPLICANT: E. I. du Pont de Nemours and Company

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

; FILE REFERENCE: BBI339 PCT

; CURRENT APPLICATION NUMBER: US/09/857,581

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769

; PRIOR FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: 60/144,783

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 60/156,094

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 65

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER

US-09-857-581-65

Query Match 76.0%; Score 11.4; DB 6; Length 25;  
Best Local Similarity 92.3%; Pred. No. 4.2e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 acccaggtgagtct 15  
|||||

Db 17 CCCAGGTGAGTTT 5

RESULT 4

US-09-801-274-1705/c

; Sequence 1705, Application US/09801274

; GENERAL INFORMATION:

; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.

; APPLICANT: Lander, Eric S.

; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS

; FILE REFERENCE: 2825.2009-001

; CURRENT APPLICATION NUMBER: US/09/801,274

; CURRENT FILING DATE: 2001-03-07

; PRIOR APPLICATION NUMBER: US 60/187,510

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 60/206,129

; PRIOR FILING DATE: 2000-05-22

; NUMBER OF SEQ ID NOS: 1802

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1705

; LENGTH: 31

; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-801-274-1705

Query Match 76.0%; Score 11.4; DB 6; Length 31;  
Best Local Similarity 92.3%; Pred. No. 4.3e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 cccaggtgagtct 15  
|||||

Db 14 CCCAGCTGAGTCT 2

RESULT 5

US-09-794-384A-10

; Sequence 10, Application US/09794384A

; GENERAL INFORMATION:

; APPLICANT: Dellaporta, Stephen L.

; APPLICANT: Moreno, Maria A.

; APPLICANT: Yale University

; TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate

; FILE REFERENCE: 44574-5078-US

; CURRENT APPLICATION NUMBER: US/09/794,384A

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: US 60/185,524

; PRIOR FILING DATE: 2000-02-28

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 27

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: 5' PCR primer  
US-09-794-384A-10

Query Match 72.0%; Score 10.8; DB 7; Length 27;  
Best Local Similarity 85.7%; Pred. No. 9.7e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15  
|||||

Db 1 acccaggtgagttt 14

RESULT 6

US-09-406-643-4/c

; Sequence 4, Application US/09406643

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Ludwig, Janos

; APPLICANT: Sproat, Brian

; APPLICANT: Beigelman, Leonid

; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity

; FILE REFERENCE: MBHB00-874-A (237/197)

; CURRENT APPLICATION NUMBER: US/09/406,643

; CURRENT FILING DATE: 1999-09-27

; PRIOR APPLICATION NUMBER: US 08/879,078

; PRIOR FILING DATE: 1997-06-19

; PRIOR APPLICATION NUMBER: US 08/878,640

; NUMBER OF SEQ ID NOS: 2606

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-406-643-4

Query Match 69.3%; Score 10.4; DB 5; Length 15;

Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccaggtgagtc 15  
||||||| ||||  
Db 15 CCAGGTGGGTCT 4

RESULT 7  
US-09-406-643-293/C  
; Sequence 293, Application US/09406643  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Ludwig, Janos  
; APPLICANT: Sproat, Brian  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity  
; FILE REFERENCE: MBH00-874-A (237/197)  
; CURRENT APPLICATION NUMBER: US/09/406,643  
; CURRENT FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 08/879,078  
; PRIOR FILING DATE: 1997-06-19  
; PRIOR APPLICATION NUMBER: US 08/878,640  
; PRIOR FILING DATE: 1997-06-19  
; NUMBER OF SEQ ID NOS: 2606  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 293  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-406-643-293

Query Match 69.3%; Score 10.4; DB 5; Length 15;  
Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccaggtgagtc 15  
||||||| ||||  
Db 14 CCAGGTGGGTCT 3

RESULT 8  
US-09-406-643-294/C  
; Sequence 294, Application US/09406643  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Ludwig, Janos  
; APPLICANT: Sproat, Brian  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity  
; FILE REFERENCE: MBH00-874-A (237/197)  
; CURRENT APPLICATION NUMBER: US/09/406,643  
; CURRENT FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 08/879,078  
; PRIOR FILING DATE: 1997-06-19  
; PRIOR APPLICATION NUMBER: US 08/878,640  
; PRIOR FILING DATE: 1997-06-19  
; NUMBER OF SEQ ID NOS: 2606  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 294  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-406-643-294

Query Match 69.3%; Score 10.4; DB 5; Length 15;  
Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccaggtgagtc 15  
||||||| ||||

Db 13 CCAGGTGGGTCT 2

RESULT 9  
US-09-866-108-7712  
; Sequence 7712, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 7712  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7712

Query Match 69.3%; Score 10.4; DB 6; Length 17;  
Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ccaggtgagtc 14  
||||||| ||||  
Db 6 cctaggtgagtc 17

RESULT 10  
US-09-866-108-7713  
; Sequence 7713, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.

Query Match 69.3%; Score 10.4; DB 6;  
Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels

RESULT 12  
US-09-866-108-7715  
; Sequence 7715, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; FILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; TITLE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866.108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 7715  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7715

Query Match 69.3%; Score 10.4; DB 6; Length 17;  
Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cccaggtgagtc 14  
|||  
Db 3 cctaggtgagtc 14

## RESULT 13

US-09-866-108-7716  
; Sequence 7716, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; SOFTWARE: Aeomica Sequence Listing Engine

; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 7716  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7716

Query Match 69.3%; Score 10.4; DB 6; Length 17;  
Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cccaggtgagtc 14  
|||  
Db 2 cctaggtgagtc 13

## RESULT 14

US-09-866-108-7717  
; Sequence 7717, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine

```
; SEQ ID NO 7717
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7717

Query Match      69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 cccaggtgagtc 14
   || |||||
Db 1 cctaggtgagtc 12

RESULT 15
US-09-927-796-165
; Sequence 165, Application US/09927796
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2531R1C1
; CURRENT APPLICATION NUMBER: US/09/927,796
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/067411
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/069862
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/095929
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/097978
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/108867
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112851
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/119965
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/123972
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/133459
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140653
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/149395
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151689
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 08/625328
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 08/710802
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 08/800699
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: 08/828683
; PRIOR FILING DATE: 1997-03-31
; PRIOR APPLICATION NUMBER: 08/829270
; PRIOR FILING DATE: 1997-03-31
; PRIOR APPLICATION NUMBER: 08/928069
; PRIOR FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: 08/934494
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 09/143068
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/143707
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/151889
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 09/169104
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: 09/202089
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: 09/254311
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/304003
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423844
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 09/511133
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/511631
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/664610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/665350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/690169
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/690189
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-18
; PRIOR APPLICATION NUMBER: 09/866034
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;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 09/872035  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: 09/884733  
;; PRIOR FILING DATE: 2001-06-19  
;; PRIOR APPLICATION NUMBER: 09/886342  
;; PRIOR FILING DATE: 2001-06-19  
;; PRIOR APPLICATION NUMBER: 09/866028  
;; PRIOR FILING DATE: 2001-08-25  
;; PRIOR APPLICATION NUMBER: PCT/US97/05230  
;; PRIOR FILING DATE: 1997-03-31  
;; PRIOR APPLICATION NUMBER: PCT/US98/19094  
;; PRIOR FILING DATE: 1998-09-14  
;; PRIOR APPLICATION NUMBER: PCT/US98/19330  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: PCT/US98/21407  
;; PRIOR FILING DATE: 1998-10-09  
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;; PRIOR FILING DATE: 1998-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US99/05028  
;; PRIOR FILING DATE: 1999-03-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: 1999-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/20111  
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;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
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;; PRIOR FILING DATE: 1999-12-01  
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;; PRIOR FILING DATE: 2000-02-22  
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;; PRIOR FILING DATE: 2000-03-02  
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;; PRIOR FILING DATE: 2000-07-28  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: 2000-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US01/17800  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: PCT/US01/19692  
;; PRIOR FILING DATE: 2001-06-20  
;; PRIOR APPLICATION NUMBER: PCT/US01/21066  
;; PRIOR FILING DATE: 2001-06-29  
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;; PRIOR FILING DATE: 2001-07-09  
;; NUMBER OF SEQ ID NOS: 258  
;; SEQ ID NO 165  
;; LENGTH: 19

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Best Local Similarity 91.7%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 cccaggtgagtc 14  
  || |||||  
Db 5 ccaaggtgagtc 16

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Job time: 17670 sec

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:20 ; Search time 17695.9 Seconds  
(without alignments)  
12.526 Million cell updates/sec

Title: US-09-757-100B-31

Perfect score: 15

Sequence: 1 taccacagtgagtct 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	15	100.0	15	17	US-09-377-310-31
3	15	100.0	15	29	US-09-757-100B-31
4	15	100.0	20	1	PCT-US00-18999-11
5	15	100.0	20	17	US-09-377-310-11
6	15	100.0	20	29	US-09-757-100B-11
7	13.4	89.3	25	26	US-09-660-220-7111
8	12.4	82.7	21	3	US-07-918-259-7
9	12.4	82.7	25	55	US-60-233-166-72838
10	12.4	82.7	25	55	US-60-233-166-188071
11	12.4	82.7	25	55	US-60-233-166-293033
12	12.4	82.7	25	55	US-60-234-017-93096
13	12.4	82.7	25	55	US-60-234-017-150700
14	12.4	82.7	25	55	US-60-234-017-150701
15	12.4	82.7	25	55	US-60-234-017-49268
16	12.4	82.7	25	55	US-60-234-017-558705
17	12.4	82.7	25	55	US-60-234-017-558707
18	12.4	82.7	28	31	US-09-872-852-17
19	12	80.0	25	26	US-09-660-220-125589
20	12	80.0	25	55	US-60-233-166-20465
21	12	80.0	25	55	US-60-233-166-417490
22	12	80.0	32	15	US-09-180-245-69
23	11.8	78.7	25	55	US-60-233-166-61896
24	11.8	78.7	25	55	US-60-233-166-107363
25	11.8	78.7	25	55	US-60-233-166-111592
26	11.8	78.7	25	55	US-60-233-166-320910
27	11.8	78.7	25	55	US-60-233-166-334434
28	11.8	78.7	25	55	US-60-233-166-379370
29	11.8	78.7	25	55	US-60-233-357-9034
30	11.8	78.7	25	55	US-60-233-620-119428
31	11.8	78.7	25	55	US-60-234-017-22543
32	11.8	78.7	25	55	US-60-234-017-22546
33	11.8	78.7	25	55	US-60-234-017-22548
34	11.8	78.7	25	55	US-60-234-017-142091
35	11.8	78.7	25	55	US-60-234-017-147526
36	11.8	78.7	25	55	US-60-234-017-270612
37	11.8	78.7	25	55	US-60-234-017-271439
38	11.8	78.7	25	55	US-60-234-017-296787
39	11.8	78.7	25	55	US-60-234-017-365211
40	11.8	78.7	25	55	US-60-234-017-536140
41	11.8	78.7	25	55	US-60-234-017-536143
42	11.8	78.7	25	55	US-60-234-017-536147
43	11.8	78.7	34	16	US-09-214-151-3
44	11.8	78.7	48	18	US-09-404-520-33931
45	11.4	76.0	18	3	US-07-674-366-33

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-31  
; Sequence 31, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-31

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taccagggtgagtct 15  
Db 1 taccagggtgagtct 15

RESULT 2  
US-09-377-310-31  
; Sequence 31, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-31

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 taccagggtgagtct 15

RESULT 3  
US-09-757-100B-31  
; Sequence 31, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-31

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 taccagggtgagtct 15

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; Sequence 11, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-11

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Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taccagggtgagtct 15  
Db 3 taccagggtgagtct 17

RESULT 5  
US-09-377-310-11  
; Sequence 11, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.



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; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 293033
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI639536
US-60-233-166-293033

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Best Local Similarity 92.9%; Pred. No. 8.5e+03;
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Db 23 TACCCAGGTCAGTC 10

RESULT 12
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; Sequence 93096, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI854595
US-60-234-017-93096

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Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 19 TACCCAGGTCGTC 6

RESULT 13
US-60-234-017-150700
; Sequence 150700, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI849180
US-60-234-017-150700

; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819408
US-60-233-166-72838

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Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 10 accaaggtagtct 23

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US-60-233-166-188071
; Sequence 188071, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188071
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA963963
US-60-233-166-188071

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Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 4 accaaggtagtct 17

RESULT 11
US-60-233-166-293033/c
; Sequence 293033, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
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Best Local Similarity 92.9%; Pred. No. 8.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 10 accaagtgagtct 23

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; Sequence 150701, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; TITLE OF INVENTION: musculus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 150701  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF849180  
US-60-234-017-150701

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 8.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15  
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Db 7 accaagtgagtct 20

RESULT 15  
US-60-234-017-449268  
; Sequence 449268, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; TITLE OF INVENTION: musculus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 449268  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AW123353  
US-60-234-017-449268

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 8.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15  
| | | | | | | | | |  
Db 2 acccaggtgagtct 15

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:20 ; Search time 17695.9 Seconds  
(without alignments)  
12.526 Million cell updates/sec

Title: US-09-757-100B-30  
Perfect score: 15  
Sequence: 1 taagcagctgccatt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues  
Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq:\*

10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq:\*

11: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq:\*

12: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq:\*

13: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq:\*

14: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq:\*

15: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq:\*

16: /cgn2\_6/ptodata/1/pna/US092\_COMB.seq:\*

17: /cgn2\_6/ptodata/1/pna/US093\_COMB.seq:\*

18: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq:\*

19: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq:\*

20: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq:\*

21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq:\*

22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq:\*

23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq:\*

24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq:\*

25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq:\*

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27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq:\*

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35: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq:\*

36: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq:\*

37: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq:\*

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39: /cgn2\_6/ptodata/1/pna/US099G\_COMB.seq:\*

40: /cgn2\_6/ptodata/1/pna/US099H\_COMB.seq:\*

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42: /cgn2\_6/ptodata/1/pna/US099J\_COMB.seq:\*

43: /cgn2\_6/ptodata/1/pna/US099K\_COMB.seq:\*

44: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq:\*

45: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq:\*

46: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq:\*

47: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq:\*

48: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq:\*

49: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq:\*

50: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq:\*

51: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq:\*

52: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq:\*

53: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq:\*

54: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq:\*

55: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq:\*

56: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq:\*

57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq:\*

58: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq:\*

59: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq:\*

60: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	15	1	PCT-US00-18999-30
2	15	100.0	15	17	US-09-377-310-30
3	15	100.0	15	29	US-09-757-100B-30
4	15	100.0	20	1	PCT-US00-18999-10
5	15	100.0	20	17	US-09-377-310-10
6	15	100.0	20	29	US-09-757-100B-10
7	13.4	89.3	18	7	US-08-378-761-45
8	12.4	82.7	24	1	PCT-US01-06413-8
9	12.4	82.7	25	55	US-60-234-049-76441
10	12.4	82.7	27	16	US-09-218-207-173
11	12.4	82.7	27	17	US-09-338-907-173
12	12.4	82.7	49	19	US-09-507-691-6
13	12	80.0	15	1	PCT-US01-05126-13
14	12	80.0	25	55	US-60-233-620-95891
15	12	80.0	25	55	US-60-233-620-111530
16	12	80.0	32	11	US-08-700-519F-5
17	12	80.0	32	11	US-08-700-519J-5
18	12	80.0	32	11	US-08-700-519J-5
19	12	80.0	39	16	US-09-211-424-18
20	12	80.0	47	53	US-60-216-745-4119
21	11.8	78.7	21	57	US-60-259-128-3252
22	11.8	78.7	25	55	US-60-232-638-20692
23	11.8	78.7	25	55	US-60-232-638-75827
24	11.8	78.7	25	55	US-60-233-620-13224
25	11.8	78.7	25	55	US-60-234-017-432078
26	11.8	78.7	25	55	US-60-234-017-432084
27	11.8	78.7	25	55	US-60-234-017-432087
28	11.8	78.7	25	55	US-60-234-017-432091
29	11.8	78.7	25	55	US-60-234-017-502150
30	11.8	78.7	25	55	US-60-234-049-38053
31	11.8	78.7	27	9	US-08-584-040-689
32	11.8	78.7	47	23	US-09-605-699-9769
33	11.8	78.7	50	8	US-08-475-228-486
34	11.8	78.7	50	8	US-08-475-228-487
35	11.8	78.7	50	8	US-08-482-080-486
36	11.8	78.7	50	8	US-08-482-080-487
37	11.8	78.7	50	16	US-09-270-849B-135913
38	11.8	78.7	50	17	US-09-354-947-486
39	11.8	78.7	50	17	US-09-354-947-487
40	11.6	77.3	29	17	US-09-304-232-241
41	11.4	76.0	19	5	US-08-165-306A-7
42	11.4	76.0	20	7	US-08-309-335A-1215
43	11.4	76.0	20	9	US-08-531-241A-1215
44	11.4	76.0	20	12	US-08-832-658-4
45	11.4	76.0	20	16	US-09-263-959-1215

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-30  
; Sequence 30, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-30

Query Match 100.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 taagcagctgccatt 15  
Db 1 taagcagctgccatt 15  
|||||  
RESULT 2  
US-09-377-310-30  
; Sequence 30, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: US/09/377,310A  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-30

Query Match 100.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 taagcagctgccatt 15  
Db 1 taagcagctgccatt 15  
|||||  
RESULT 3  
US-09-757-100B-30  
; Sequence 30, Application US/09757100B  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US/09/757,100B  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-30

Query Match 100.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 taagcagctgccatt 15  
Db 1 taagcagctgccatt 15  
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RESULT 4  
PCT-US00-18999-10  
; Sequence 10, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-10

Query Match 100.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 taagcagctgccatt 15  
Db 1 taagcagctgccatt 15  
|||||  
RESULT 5  
US-09-377-310-10  
; Sequence 10, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-10

GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US/09/757,100B  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-30

Query Match 100.0%; Score 15; DB 29; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15  
Db 1 taagcagctgccatt 15  
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RESULT 4  
PCT-US00-18999-10  
; Sequence 10, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-10

Query Match 100.0%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15  
Db 3 taagcagctgccatt 17  
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RESULT 5  
US-09-377-310-10  
; Sequence 10, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.

APPLICANT: Gaarde, William A.  
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
FILE REFERENCE: ISPH-0389  
CURRENT APPLICATION NUMBER: US/09/377,310A  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: antisense sequence  
US-09-377-310-10

Query Match 100.0%; Score 15; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15  
|||||

Db 3 taagcagctgccatt 17

## RESULT 6

US-09-757-100B-10  
Sequence 10, Application US/09757100B  
GENERAL INFORMATION:  
APPLICANT: Monia, Brett P.  
APPLICANT: Gaarde, William A.  
APPLICANT: Nero, Pamela S.  
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
FILE REFERENCE: ISPH-0533  
CURRENT APPLICATION NUMBER: US/09/757,100B  
CURRENT FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: 09/377,310  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/US00/18999  
PRIOR FILING DATE: 2000-07-13  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: antisense sequence  
US-09-757-100B-10

Query Match 100.0%; Score 15; DB 29; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15  
|||||

Db 3 taagcagctgccatt 17

## RESULT 7

US-08-378-761-45/c  
Sequence 45, Application US/08378761  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
PRECUSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
PRECUSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:  
ADDRESSEE: THOMAS D. ZINDRICK  
STREET: 9002 PURDUE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268-1189  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/987927  
FILING DATE: 09-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ZINDRICK, THOMAS D  
REGISTRATION NUMBER: 32185  
REFERENCE/DOCKET NUMBER: 38272A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 636-1869  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-378-761-45

Query Match 89.3%; Score 13.4; DB 7; Length 18;  
Best Local Similarity 99.3%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15  
|||||

Db 17 TAAGCAGCTGCAATT 3

## RESULT 8

PCT-US01-06413-8/c  
Sequence 8, Application PC/TUS0106413  
GENERAL INFORMATION:  
APPLICANT: The General Hospital Corporation  
TITLE OF INVENTION: BETA NETRIN AND USES THEREOF  
FILE REFERENCE: 10287-057W01  
CURRENT APPLICATION NUMBER: PCT/US01/06413  
CURRENT FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: US 60/185,811  
PRIOR FILING DATE: 2000-02-29  
PRIOR APPLICATION NUMBER: US 60/229,893  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer for PCR  
PCT-US01-06413-8

Query Match 82.7%; Score 12.4; DB 1; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.4e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 aagcagctgccatt 15  
|||||

Db 21 AAGCAGCTGCCCTT 8

## RESULT 9

US-60-234-049-76441/c  
; Sequence 76441, Application US/60234049  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, Michael  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of  
; TITLE OF INVENTION: Escherichia coli  
; FILE REFERENCE: 3117  
; CURRENT APPLICATION NUMBER: US/60/234,049  
; EARLIER FILING DATE: 2000-09-19  
; NUMBER OF SEQ ID NOS: 141629  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76441  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank U00096  
US-60-234-049-76441

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.4e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 aagcagctgccatt 15

Db 18 AAGCTGCTGCCATT 5  
||||| |||||||

## RESULT 10

US-09-218-207-173/c  
; Sequence 173, Application US/09218207  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Ilya, Chumakov  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Prostate cancer gene  
; FILE REFERENCE: GENSET.018CPI  
; CURRENT APPLICATION NUMBER: US/09/218,207  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 08/996,306  
; EARLIER FILING DATE: 1997-12-22  
; EARLIER APPLICATION NUMBER: 60/099,658  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 578  
; SOFTWARE: Patent.pm  
; SEQ ID NO 173  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: 1..27  
; OTHER INFORMATION: amplification oligonucleotide PGIaE5b8  
US-09-218-207-173

Query Match 82.7%; Score 12.4; DB 16; Length 27;  
Best Local Similarity 92.9%; Pred. No. 1.4e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 taagcagctgccatt 14

Db 24 TAAGCATCTGCCAT 11  
||||| |||||||

## RESULT 11

US-09-338-907-173/c  
; Sequence 173, Application US/09338907  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Ilya, Chumakov  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: PROSTATE CANCER GENE  
; FILE REFERENCE: GENSET.18CPICP  
; CURRENT APPLICATION NUMBER: US/09/338,907  
; CURRENT FILING DATE: 1999-06-23  
; EARLIER APPLICATION NUMBER: 08/996,306  
; EARLIER FILING DATE: 1997-12-22  
; EARLIER APPLICATION NUMBER: 60/099,658  
; EARLIER FILING DATE: 1998-09-09  
; EARLIER APPLICATION NUMBER: 09/218,207  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 578  
; SOFTWARE: Patent.pm  
; SEQ ID NO 173  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: 1..27  
; OTHER INFORMATION: amplification oligonucleotide PGIaE5b8  
US-09-338-907-173

Query Match 82.7%; Score 12.4; DB 17; Length 27;  
Best Local Similarity 92.9%; Pred. No. 1.4e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 taagcagctgccatt 14

Db 24 TAAGCATCTGCCAT 11  
||||| |||||||

## RESULT 12

US-09-507-691-6/c  
; Sequence 6, Application US/09507691  
; GENERAL INFORMATION:  
; APPLICANT: ISHIKAWA, Tetsuya  
; APPLICANT: KITAJIMA, Takashi  
; TITLE OF INVENTION: COLLAGEN-BINDING PHYSIOLOGICALLY ACTIVE POLYPEPTIDE  
; FILE REFERENCE: 029650-087  
; CURRENT APPLICATION NUMBER: US/09/507,691  
; CURRENT FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: JP 11-041913  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: JP 11-311364  
; PRIOR FILING DATE: 1999-11-01  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR sense  
; OTHER INFORMATION: primer for human fibronectin collagen-binding  
; OTHER INFORMATION: domain  
US-09-507-691-6

Query Match 82.7%; Score 12.4; DB 19; Length 49;  
Best Local Similarity 92.9%; Pred. No. 1.6e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 taagcagctgccatt 14

Db 31 TAACAGCTGCCAT 18  
||| |||||||

RESULT 13  
PCT-US01-05126-13/c  
; Sequence 13, Application PC/TUS0105126  
; GENERAL INFORMATION:  
; APPLICANT: Denton, Richard R  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Chew, Anne  
; APPLICANT: Choi, Julie  
; APPLICANT: Stephens, J. Claiborne  
; APPLICANT: Genessee Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Haplotypes of the PON1 Gene  
; FILE REFERENCE: PONIPT  
; CURRENT APPLICATION NUMBER: PCT/US01/05126  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 60/182,930  
; PRIOR FILING DATE: 2000-02-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PCT-US01-05126-13

Query Match 80.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.2e+04;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 aagcagctgccatt 15  
|:|||||||  
Db 15 AWGAGCTGGCATT 2

Search completed: October 2, 2001, 21:50:20.  
Job time: 24533 sec

RESULT 14  
US-60-233-620-95891  
; Sequence 95891, Application US/60233620  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of  
; Arabidopsis thaliana  
; FILE REFERENCE: 3116  
; CURRENT APPLICATION NUMBER: US/60/233,620  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 131820  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 95891  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AC007591  
US-60-233-620-95891

Query Match 80.0%; Score 12; DB 55; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgcc 12  
|:|||||||  
Db 13 taagcagctgcc 24

RESULT 15  
US-60-233-620-111530  
; Sequence 111530, Application US/60233620  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of  
; Arabidopsis thaliana  
; FILE REFERENCE: 3116  
; CURRENT APPLICATION NUMBER: US/60/233,620  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 131820  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 111530  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AL035394  
US-60-233-620-111530

Query Match 80.0%; Score 12; DB 55; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgcc 12  
|:|||||||  
Db 10 taagcagctgcc 21

Search completed: October 2, 2001, 21:50:20.  
Job time: 24533 sec

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;  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7017

Query Match 80.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aagcagctgccca 13  
|||||  
DB 17 AAGCAGCTGCCA 6

## RESULT 2

US-09-866-108-7018/c  
; Sequence 7018, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 7018  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7018

Query Match 80.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aagcagctgccca 13  
|||||  
DB 16 AAGCAGCTGCCA 5

## RESULT 3

US-09-866-108-7019/c  
; Sequence 7019, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 7019  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7019

Query Match 80.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aagcagctgccca 13  
|||||  
DB 15 AAGCAGCTGCCA 4

## RESULT 4

US-09-866-108-7020/c  
; Sequence 7020, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong



```
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7020

Query Match      80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 aagcagctgcca 13
        |||||
Db      14 AAGCAGCTGCCA 3

RESULT 5
US-09-866-108-7021/c
; Sequence 7021, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7020

Query Match      80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 aagcagctgcca 13
        |||||
Db      14 AAGCAGCTGCCA 3

RESULT 6
US-09-866-108-7022/c
; Sequence 7022, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7021
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7021
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; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
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; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 7022  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7022

Query Match 80.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 aagcagctgccca 13  
|||||  
Db 12 AAGCAGCTGCCA 1

RESULT 7  
US-09-866-108-11909/c  
; Sequence 11909, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOmica-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 11909  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-11909

Query Match 80.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 aagcagctgccca 13  
|||||  
Db 25 AAGCAGCTGCCA 14

RESULT 8  
US-09-866-108-11910/c  
; Sequence 11910, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOmica-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 11910  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-11910

Query Match 80.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 aagcagctgccca 13  
| | | | | | | | | |  
Db 24 AAGCAGCTGCCA 13

RESULT 9  
US-09-866-108-11911/c  
; Sequence 11911, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AECOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866.108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 11911  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-11911

Query Match 80.0%; Score 12; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 aagcagctgccca 13  
| | | | | | | | | |  
Db 23 AAGCAGCTGCCA 12

RESULT 10  
US-09-866-108-11912/c  
; Sequence 11912, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AECOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866.108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
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; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 11912  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-11912

Query Match 80.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 aagcagctgccca 13  
| | | | | | | | | |  
Db 22 AAGCAGCTGCCA 11

RESULT 11  
US-09-866-108-11913/c

```
; Sequence 11913, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11913
```

```
Query Match 80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 aagcagctgccca 13
Db 21 AAGCAGCTGCCA 10
|||||
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```
RESULT 12
US-09-866-108-11914/c
; Sequence 11914, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
```

```
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11914
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11914
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```
Query Match 80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 2 aagcagctgccca 13
Db 20 AAGCAGCTGCCA 9
|||||
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```
RESULT 13
US-09-866-108-11915/c
; Sequence 11915, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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Wed Oct 3 08:30:32 2001

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aequica Sequence Listing Engine
; SEQ ID NO 11915
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11915

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Query Match 80.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels

Qy 2 aagcagctgcca 13  
          |||||  
Db 19 AAGCAGCTGCCA 8

RESULT 14  
US-09-866-108-11916/c  
; Sequence 11916, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: FENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOICA-7  
; CURRENT APPLICATION NUMBER: US/09/866.108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
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; PRIOR APPLICATION NUMBER: PCT/US01/00668

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? PRIOR FILING DATE: 2001-01-30
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? PRIOR APPLICATION NUMBER: PCT/US01/006670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 60/266,860
? PRIOR FILING DATE: 2001-02-05
? NUMBER OF SEQ ID NOS: 15752
? SEQ ID NO 11916
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-866-108-11916

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Query Match	80.0%;	Score 12;	DB 6;	Length 25;
Best-Local Similarity	100.0%;	Pred. No. 2.9e+03;		
Matches 12;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 2 aagcagctgcca 13  
|||||  
Db 18 AAGCAGCTGCCA 7

RESULT 15

US-09-866-108-11917/c

> Sequence 11917, Application US/09866108

> GENERAL INFORMATION:

> APPLICANT: GU, Yizhong

> APPLICANT: JI, Yongqiang

> APPLICANT: PENN, Sharron G.

> APPLICANT: HANZEL, David K.

> APPLICANT: RANK, David R.

> APPLICANT: CHEN, Wensheng

> APPLICANT: SHANNON, Mark

> TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

> FILE REFERENCE: AEOmica-7

> CURRENT APPLICATION NUMBER: US/09/866,108

> CURRENT FILING DATE: 2001-05-25

> PRIOR APPLICATION NUMBER: US 60/207,456

> PRIOR FILING DATE: 2000-05-26

> PRIOR APPLICATION NUMBER: GB 2463.6

> PRIOR FILING DATE: 2000-10-04

> PRIOR APPLICATION NUMBER: US 60/236,359

> PRIOR FILING DATE: 2000-09-27

> PRIOR APPLICATION NUMBER: PCT/US01/00666

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00667

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00664

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00669

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00665

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00668

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00663

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00662

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00661

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: PCT/US01/00670

> PRIOR FILING DATE: 2001-01-30

> PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 11917  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-11917

Query Match 80.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 aagcagctgccca 13  
Db 17 AAGCAGCTGCCCA 6

Search completed: October 2, 2001, 16:55:07  
Job time: 17670 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:19 ; Search time 17695.9 Seconds  
(without alignments)  
12.526 Million cell updates/sec

Title: US-09-757-100B-23

Perfect score: 15

Sequence: 1 gcgggctcacagtgg 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /cgn2\_6/ptodata/1/pna/US0612\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/US0613\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq:\*

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27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq:\*

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41: /cgn2\_6/ptodata/1/pna/US099\_COMB.seq:\*

42: /cgn2\_6/ptodata/1/pna/US099\_COMB.seq:\*

43: /cgn2\_6/ptodata/1/pna/US099\_COMB.seq:\*

44: /cgn2\_6/ptodata/1/pna/US06012\_COMB.seq:\*

45: /cgn2\_6/ptodata/1/pna/US06013\_COMB.seq:\*

46: /cgn2\_6/ptodata/1/pna/US06014\_COMB.seq:\*

47: /cgn2\_6/ptodata/1/pna/US06015\_COMB.seq:\*

48: /cgn2\_6/ptodata/1/pna/US06016\_COMB.seq:\*

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51: /cgn2\_6/ptodata/1/pna/US06019\_COMB.seq:\*

52: /cgn2\_6/ptodata/1/pna/US06020\_COMB.seq:\*

53: /cgn2\_6/ptodata/1/pna/US06021\_COMB.seq:\*

54: /cgn2\_6/ptodata/1/pna/US06022\_COMB.seq:\*

55: /cgn2\_6/ptodata/1/pna/US06023\_COMB.seq:\*

56: /cgn2\_6/ptodata/1/pna/US06024\_COMB.seq:\*

57: /cgn2\_6/ptodata/1/pna/US06025\_COMB.seq:\*

58: /cgn2\_6/ptodata/1/pna/US06026\_COMB.seq:\*

59: /cgn2\_6/ptodata/1/pna/US06027\_COMB.seq:\*

60: /cgn2\_6/ptodata/1/pna/US06028\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	1	PCT-US000-18999-23
2	15	100.0	15	17	US-09-377-310-23
3	15	100.0	15	29	US-09-757-100B-23
4	15	100.0	20	1	PCT-US000-18999-3
5	15	100.0	20	17	US-09-377-310-3
6	15	100.0	20	29	US-09-757-100B-3
7	12.4	82.7	25	26	US-09-660-220-37375
8	12.4	82.7	25	26	US-09-660-220-37376
9	12.4	82.7	25	26	US-09-660-220-37377
10	12.4	82.7	25	55	US-60-233-166-136549
11	12.4	82.7	25	55	US-60-233-166-229423
12	12.4	82.7	25	55	US-60-233-166-296555
13	12.4	82.7	25	55	US-60-233-357-1753
14	12.4	82.7	25	55	US-60-234-017-297601
15	12	80.0	25	55	US-60-233-166-279728
16	12	80.0	25	55	US-60-233-166-386944
17	12	80.0	25	55	US-60-233-166-402639
18	11.8	78.7	20	11	US-08-778-052-157
19	11.8	78.7	21	7	US-08-339-207-89
20	11.8	78.7	24	15	US-09-177-306-52
21	11.8	78.7	25	55	US-60-233-166-185790
22	11.8	78.7	25	55	US-60-233-166-235736
23	11.8	78.7	25	55	US-60-234-017-10846
24	11.8	78.7	25	55	US-60-234-017-42928
25	11.8	78.7	25	55	US-60-234-017-55657
26	11.8	78.7	25	55	US-60-234-017-73527
27	11.8	78.7	25	55	US-60-234-017-273976
28	11.8	78.7	25	55	US-60-234-017-376806
29	11.8	78.7	25	55	US-60-234-017-376813
30	11.8	78.7	31	9	US-08-548-059-4
31	11.8	78.7	31	14	US-09-006-298-11
32	11.8	78.7	40	9	US-08-594-866-2
33	11.8	78.7	44	1	PCT-US000-00456-83
34	11.8	78.7	47	16	US-09-218-207-282
35	11.8	78.7	47	17	US-09-338-907-282
36	11.4	76.0	17	29	US-09-724-389-56
37	11.4	76.0	18	1	PCT-US99-16219-17
38	11.4	76.0	22	8	US-09-387-341-160
39	11.4	76.0	22	8	US-08-445-289-25
40	11.4	76.0	25	26	US-09-660-080-7906
41	11.4	76.0	25	26	US-09-660-220-14258
42	11.4	76.0	25	26	US-09-660-220-25361
43	11.4	76.0	25	26	US-09-660-220-68034
44	11.4	76.0	25	26	US-09-660-220-136997
45	11.4	76.0	25	55	US-60-234-049-78752

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-23  
; Sequence 23, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-23

Query Match 100.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 gcgggctcacagtgg 15  
Db 1 gcgggctcacagtgg 15  
|||||

RESULT 2  
US-09-377-310-23  
; Sequence 23, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-23

Query Match 100.0%; Score 15; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 gcgggctcacagtgg 15  
Db 1 gcgggctcacagtgg 15  
|||||

RESULT 3  
US-09-757-100B-23  
; Sequence 23, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-23

Query Match 100.0%; Score 15; DB 29; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15  
Db 1 gcgggctcacagtgg 15  
|||||

RESULT 4  
PCT-US00-18999-3  
; Sequence 3, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-3

Query Match 100.0%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 gcgggctcacagtgg 15  
Db 3 gcgggctcacagtgg 17  
|||||

RESULT 5  
US-09-377-310-3  
; Sequence 3, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.



; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-3

Query Match 100.0%; Score 15; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 qcgggctcacagtgg 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 qcgggctcacagtgg 17

RESULT 6  
US-09-757-100b-3  
; Sequence 3, Application US/09757100B  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100b-3

Query Match 100.0%; Score 15; DB 29; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 qcgggctcacagtgg 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 qcgggctcacagtgg 17

RESULT 7  
US-09-660-220-37375  
; Sequence 37375, Application US/09660220  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann et al.  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Human  
; FILE REFERENCE: 3102.1  
; CURRENT APPLICATION NUMBER: US/09/660,220  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/164,973

; PRIOR FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 140981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37375  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank L11931  
US-09-660-220-37375

Query Match 82.7%; Score 12.4; DB 26; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 12 cgggctcacagtgg 25

RESULT 8  
US-09-660-220-37376  
; Sequence 37376, Application US/09660220  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann et al.  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Human  
; FILE REFERENCE: 3102.1  
; CURRENT APPLICATION NUMBER: US/09/660,220  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/164,973  
; PRIOR FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 140981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37376  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank L11931  
US-09-660-220-37376

Query Match 82.7%; Score 12.4; DB 26; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 8 cgggctcacagtgg 21

RESULT 9  
US-09-660-220-37377  
; Sequence 37377, Application US/09660220  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann et al.  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Human  
; FILE REFERENCE: 3102.1  
; CURRENT APPLICATION NUMBER: US/09/660,220  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/164,973  
; PRIOR FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 140981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37377  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank L11931  
US-09-660-220-37377

US-09-660-220-37377

Query Match 82.7%; Score 12.4; DB 26; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
|||||

Db 4 cgggctcacagtgg 17

RESULT 10

US-60-232-638-136549/c  
; Sequence 136549, Application US/60232638  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
; FILE REFERENCE: 3110  
; CURRENT APPLICATION NUMBER: US/60/232,638  
; NUMBER OF SEQ ID NOS: 138410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 136549  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces Cerevisiae  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SGD YPR119W  
US-60-232-638-136549

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 14  
|||||

Db 20 GCGGGCACACAGTG 7

RESULT 11

US-60-233-166-229423  
; Sequence 229423, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; NUMBER OF SEQ ID NOS: 2000-10-24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 229423  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF016901  
US-60-233-166-229423

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
|||||

Db 1 cgggctcacagtgg 14

RESULT 12

US-60-233-166-296555/c  
; Sequence 296555, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; NUMBER OF SEQ ID NOS: 2000-10-24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 296555  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF016901  
US-60-233-166-296555

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
|||||

Db 23 GCGGGCACACAGTG 10

RESULT 13

US-60-233-357-1753  
; Sequence 1753, Application US/60233357  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3114  
; CURRENT APPLICATION NUMBER: US/60/233,357  
; NUMBER OF SEQ ID NOS: 21305  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1753  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF016901  
US-60-233-357-1753

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
|||||

Db 1 cgggctcacagtgg 14

RESULT 14

US-60-234-017-297601/c  
; Sequence 297601, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 297601  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AI854291  
US-60-234-017-297601

Query Match 82.7%; Score 12.4; DB 55; Length 25;  
Best Local Similarity 92.9%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
||| |||||  
Db 20 CGGACTCAGGTGG 7

RESULT 15  
US-60-233-166-279728/c  
; Sequence 279728, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; TITLE OF INVENTION: Genome  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 279728  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AI639107  
US-60-233-166-279728

Query Match 80.0%; Score 12; DB 55; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggctcacagtgg 15  
||| |||||  
Db 21 GGCTCAGGTGG 10

Search completed: October 2, 2001, 21:50:20  
Job time: 24533 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:06 ; Search time 2173.58 Seconds  
(without alignments)  
14.467 Million cell updates/sec

Title: US-09-757-100B-23

Perfect score: 15

Sequence: 1 gcgggtcacagtgg 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/2/pna/PTCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq1.\*
- 7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq2.\*
- 8: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
c 1	11.4	76.0	18	7	US-09-787-252-17
2	11.4	76.0	25	7	US-09-735-271-2037
c 3	11.4	76.0	40	7	US-09-735-271-1558
4	10.4	69.3	17	6	US-09-866-108-10732
5	10.4	69.3	17	6	US-09-866-108-10733
6	10.4	69.3	17	6	US-09-866-108-10734
7	10.4	69.3	17	6	US-09-866-108-10735
8	10.4	69.3	17	6	US-09-866-108-10736
9	10.4	69.3	17	6	US-09-866-108-10737
c 10	10.4	69.3	18	5	US-09-925-548-93
11	10.4	69.3	20	5	US-09-827-383-1980
c 12	10.4	69.3	21	6	US-09-765-081-111
13	10.4	69.3	25	6	US-09-866-108-15624
14	10.4	69.3	25	6	US-09-866-108-15625
15	10.4	69.3	25	6	US-09-866-108-15626
16	10.4	69.3	25	6	US-09-866-108-15627
17	10.4	69.3	25	6	US-09-866-108-15628
18	10.4	69.3	25	6	US-09-866-108-15629
19	10.4	69.3	25	6	US-09-866-108-15630
20	10.4	69.3	25	6	US-09-866-108-15631
21	10.4	69.3	25	6	US-09-866-108-15632
22	10.4	69.3	25	6	US-09-866-108-15633
23	10.4	69.3	25	6	US-09-866-108-15634
24	10.4	69.3	25	6	US-09-866-108-15635
25	10.4	69.3	25	6	US-09-866-108-15636

```

26 10.4 69.3 25 6 US-09-866-108-15637, A
27 10.4 69.3 29 7 US-09-735-271-1792
28 10.4 69.3 31 6 US-09-801-274-629
29 10.4 69.3 36 5 US-09-245-026-21
30 10.4 69.3 36 6 US-09-245-025-21
c 31 10.4 69.3 37 5 US-09-708-690-20444
32 10.4 69.3 48 7 US-09-864-785-3509
c 33 10.2 68.0 17 5 US-09-708-690-9309
34 10.2 68.0 17 6 US-09-866-108-2229
35 10.2 68.0 17 6 US-09-866-108-2230
36 10.2 68.0 17 6 US-09-866-108-2231
37 10.2 68.0 20 7 US-09-825-497-23
38 10.2 68.0 25 6 US-09-879-341-12
39 10.2 68.0 25 6 US-09-866-108-5158
40 10.2 68.0 25 6 US-09-866-108-5159
41 10.2 68.0 25 6 US-09-866-108-5160
42 10.2 68.0 25 6 US-09-866-108-5161
43 10.2 68.0 25 6 US-09-866-108-5162
44 10.2 68.0 25 6 US-09-866-108-5163
45 10.2 68.0 25 6 US-09-866-108-5164

```

#### ALIGNMENTS

```

RESULT 1
US-09-787-252-17/c
; Sequence 17, Application US/09787252
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF RHO G EXPRESSION
; FILE REFERENCE: RTSP-Q106
; CURRENT APPLICATION NUMBER: US/09/787,252
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/161,015
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-787-252-17

```

```

Query Match 76.0%; Score 11.4; DB 7; Length 18;
Best Local Similarity 92.3%; Pred. No. 5.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 2 cggggtcacagtg 14
      ||||| |||||
Db 17 CGGGGCGCACAGTG 5

```

```

RESULT 2
US-09-735-271-2037
; Sequence 2037, Application US/09735271
; GENERAL INFORMATION:
; APPLICANT: Daly, Mark J.
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Lander, Eric S.
; APPLICANT: Rioux, John
; APPLICANT: Siminovich, Kathy
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS
; FILE REFERENCE: 2825.1025-002
; CURRENT APPLICATION NUMBER: US/09/735,271
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/170,257
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-271-2037
```

```
Query Match 76.0%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 5.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 cggggtcacagt 14
   ||| ||||| |||
```

```
Db 4 cgggtcacagt 16
```

## RESULT 3

```
US-09-735-271-1558/c
; Sequence 1558, Application US/09735271
; GENERAL INFORMATION:
; APPLICANT: Daly, Mark J.
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Lander, Eric S.
; APPLICANT: Rioux, John
; APPLICANT: Siminovich, Kathy
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS
; FILE REFERENCE: 2825.1025-002
; CURRENT APPLICATION NUMBER: US/09/735,271
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/170,257
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1558
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(40)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1558
```

```
Query Match 76.0%; Score 11.4; DB 7; Length 40;
Best Local Similarity 92.3%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 gcggggtcacagt 13
   ||||| ||||| |||
```

```
Db 35 GCGGGGTCACT 23
```

## RESULT 4

```
US-09-866-108-10732
; Sequence 10732, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10732
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10732
```

```
Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 ggggtcacagt 14
   ||||| |||||
```

```
Db 6 ggggtcacagt 17
```

## RESULT 5

```
US-09-866-108-10733
; Sequence 10733, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
```

; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 10733  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-10733

Query Match 69.3%; Score 10.4; DB 6; Length 17;  
Best Local Similarity 91.7%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gggtccacagt 14  
||||| |||||  
Db 5 gggtccacagt 16

RESULT 6  
US-09-866-108-10734  
; Sequence 10734, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
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; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 10734  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-10734

Query Match 69.3%; Score 10.4; DB 6; Length 17;  
Best Local Similarity 91.7%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gggtccacagt 14  
||||| |||||  
Db 4 gggtccacagt 15

RESULT 7  
US-09-866-108-10735  
; Sequence 10735, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
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; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine





; APPLICANT: Dedhar, Shoukat  
; APPLICANT: Hannigan, Greg  
; APPLICANT: Yee, Arthur  
; TITLE OF INVENTION: INTEGRIN-LINKED KINASE AND ITS USES  
; FILE REFERENCE: KINE001CIP4  
; CURRENT APPLICATION NUMBER: US/09/925,548  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 09/390,425  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 09/035,706  
; PRIOR FILING DATE: 1998-03-05  
; PRIOR APPLICATION NUMBER: 08/955,841  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 08/752,345  
; PRIOR FILING DATE: 1996-11-19  
; PRIOR APPLICATION NUMBER: 60/009,074  
; PRIOR FILING DATE: 1995-12-21  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 93  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-548-93

Query Match 69.3%; Score 10.4; DB 5; Length 18;  
Best Local Similarity 91.7%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 gcgggctcacag 12  
|||||||  
Db 13 GCGGCTCAGAG 2

RESULT 11  
US-09-827-383-1980  
; Sequence 1980, Application US/09827383  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: Macdonald Morris  
; APPLICANT: Tom Ryder  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays  
; FILE REFERENCE: 3108  
; CURRENT APPLICATION NUMBER: US/09/827,383  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: US 60/195,585  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1980  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-383-1980

Query Match 69.3%; Score 10.4; DB 5; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 2 cgggctcacagt 13  
|||||||  
Db 2 cgggctcaagt 13

RESULT 12  
US-09-765-081-111/c  
; Sequence 111, Application US/09765081  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: 2825.2008-001  
; CURRENT APPLICATION NUMBER: US/09/765,081  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,861  
; PRIOR FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 111  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-765-081-111

Query Match 69.3%; Score 10.4; DB 6; Length 21;  
Best Local Similarity 78.6%; Pred. No. 2e+04;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15  
|||||  
Db 15 CGGASTCACAGTTG 2

RESULT 13  
US-09-866-108-15624  
; Sequence 15624, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine

Query Match 69.3%; Score 10.4; DB 6; Length 25;  
Best Local Similarity 91.7%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: October 2, 2001, 16:55:06  
Job time: 17669 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:18 ; Search time 17695.9 Seconds  
(without alignments)  
16.701 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20  
Sequence: 1 catgatgcttaaaagcttac 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pna/US0612\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/US0613\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq:\*

10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq:\*

11: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq:\*

12: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq:\*

13: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq:\*

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22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq:\*

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54: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq:\*

55: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq:\*

56: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq:\*

57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq:\*

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59: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	20	100.0	20	17	US-09-377-310-20
3	20	100.0	20	29	US-09-757-100B-20
4	15	75.0	15	1	PCT-US00-18999-40
5	15	75.0	15	17	US-09-377-310-40
6	15	75.0	15	29	US-09-757-100B-40
7	14.2	71.0	25	55	US-60-234-017-498317
8	13.8	69.0	27	16	US-09-261-301C-8
9	13.6	68.0	25	55	US-60-233-166-44325
10	13.6	68.0	25	55	US-60-233-620-123801
11	13.6	68.0	25	55	US-60-234-017-564512
12	13.6	68.0	25	55	US-60-234-017-564521
13	13.6	68.0	25	55	US-60-234-017-564524
14	13.6	68.0	25	55	US-60-234-017-564527
15	13.4	67.0	25	55	US-60-232-638-137320
16	13.4	67.0	25	55	US-60-232-638-137321
17	13.4	67.0	25	55	US-60-234-017-394023
18	13.4	67.0	44	12	US-08-818-604A-5
19	13.2	66.0	22	17	US-09-345-828-8
20	13.2	66.0	25	55	US-60-232-638-82143
21	13.2	66.0	33	6	US-08-224-593-5
22	13.2	66.0	33	19	US-09-509-668-4
23	13.2	66.0	48	55	US-60-234-690-4034
24	13	65.0	25	55	US-60-232-638-68442
25	12.8	64.0	25	55	US-60-232-638-6612
26	12.8	64.0	25	55	US-60-232-638-6621
27	12.8	64.0	25	55	US-60-232-638-6632
28	12.8	64.0	25	55	US-60-233-620-46459
29	12.8	64.0	25	55	US-60-233-620-82138
30	12.8	64.0	25	55	US-60-232-620-82143
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32	12.8	64.0	25	55	US-60-234-017-421405
33	12.8	64.0	25	55	US-60-234-017-430178
34	12.8	64.0	25	55	US-60-234-049-46940
35	12.8	64.0	27	9	US-08-584-040-329
36	12.8	64.0	31	18	US-09-465-684-1490
37	12.8	64.0	32	8	US-08-484-174-14
38	12.8	64.0	34	1	PCT-US98-01468-21
39	12.8	64.0	34	14	US-09-013-896A-21
40	12.8	64.0	34	14	US-09-013-896A-21
41	12.8	64.0	34	16	US-09-216-599-25
42	12.8	64.0	34	31	US-09-827-948-21
43	12.8	64.0	36	16	US-09-216-599-39
44	12.8	64.0	42	16	US-09-216-599-23
45	12.8	64.0	42	16	US-09-216-599-24

## ALIGNMENTS

```
RESULT 1
PCT-US00-18999-20
; Sequence 20, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-20

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
Db 1 catgatgcttaaaagcttac 20
|||||

RESULT 2
US-09-377-310-20
; Sequence 20, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-20

Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
Db 1 catgatgcttaaaagcttac 20
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RESULT 3
US-09-757-100B-20
; Sequence 20, Application US/09757100B
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; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-20

Query Match      100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
Db 1 catgatgcttaaaagcttac 20
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RESULT 4
PCT-US00-18999-40
; Sequence 40, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-40

Query Match      75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagct 17
Db 1 tgatgcttaaaagct 15
|||||

RESULT 5
US-09-377-310-40
; Sequence 40, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
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; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-40

Query Match 75.0%; Score 15; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgatgcttaaaagct 17  
|||||

Db 1 tgatgcttaaaagct 15

## RESULT 6

US-09-757-100B-40  
; Sequence 40, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence

US-09-757-100B-40

Query Match 75.0%; Score 15; DB 29; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgatgcttaaaagct 17  
|||||

Db 1 tgatgcttaaaagct 15

## RESULT 7

US-60-234-017-498317  
; Sequence 498317, Application US/60234017

; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 498317  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AV213434  
US-60-234-017-498317

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atgatgcttaaaagcttac 20  
|||

Db 7 atactgcttaaaagtttac 25

## RESULT 8

US-09-261-301C-8/C  
; Sequence 8, Application US/09261301C

; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Aharonowitz, Yair  
; APPLICANT: Borovok, Ilya  
; APPLICANT: Cohen, Gerald  
; APPLICANT: \*Uziel, Orit  
; TITLE OF INVENTION: Recombinant Staphylococcus  
; TITLE OF INVENTION: Thioresoxin Reductase, And Inhibitors  
; TITLE OF INVENTION: Thereof Useful As Antimicrobial Agents  
; FILE REFERENCE: 6286.US.01  
; CURRENT APPLICATION NUMBER: US/09/261,301C  
; CURRENT FILING DATE: 1999-03-02  
; PRIOR APPLICATION NUMBER: US 60/076,525  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: C-terminal primer

US-09-261-301C-8

Query Match 69.0%; Score 13.8; DB 16; Length 27;  
Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atgatgcttaaaagctt 18  
|||

Db 20 ATCAAGCTTAAAGCTT 4

## RESULT 9

US-60-233-166-44325  
; Sequence 44325, Application US/60233166

; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 44325  
; LENGTH: 25

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; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA818914
US-60-233-166-44325

Query Match      68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
   ||||| | ||||| | ||
Db 2 catgatcataaaacatac 21

RESULT 10
US-60-233-620-123801/c
; Sequence 123801, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Arabidopsis thaliana
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123801
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X77336
US-60-233-620-123801

Query Match      68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
   ||||| | ||||| | ||
Db 20 CTTGATGCTTAAGTGCTGAC 1

RESULT 11
US-60-234-017-564512/c
; Sequence 564512, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564512
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV245764
US-60-234-017-564512

Query Match      68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
   ||||| | ||||| | ||
Db 23 CAAGATGATTGAAGGCTTAC 4

RESULT 14
US-60-234-017-564527/c
; Sequence 564527, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.

Query Match      68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
   ||||| | ||||| | ||
Db 25 CAAGATGATTGAAGGCTTAC 6

RESULT 12
US-60-234-017-564521/c
; Sequence 564521, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564521
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV245764
US-60-234-017-564521

Query Match      68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
   ||||| | ||||| | ||
Db 20 CAAGATGATTGAAGGCTTAC 1

RESULT 13
US-60-234-017-564524/c
; Sequence 564524, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV245764
US-60-234-017-564524

Query Match      68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
   ||||| | ||||| | ||
Db 23 CAAGATGATTGAAGGCTTAC 4

RESULT 14
US-60-234-017-564527/c
; Sequence 564527, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:06 ; Search time 2173.58 Seconds  
(without alignments)  
19.290 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20

Sequence: 1 catgatgcttaaaagcttac 20

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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c 4	12.2	61.0	33	5	US-09-536-784-330
c 5	12.2	61.0	33	6	US-09-765-272-330
c 6	12.2	61.0	41	8	US-60-253-378-31544
c 7	12.2	61.0	47	8	US-60-295-722-6
c 8	12.2	61.0	47	8	US-60-295-600-6
c 9	12.2	61.0	47	8	US-60-295-722-6
c 10	12.2	61.0	20	5	US-09-923-515-39
c 11	12.2	60.0	31	5	US-09-536-784-272
c 12	12.2	60.0	31	6	US-09-765-272-272
c 13	12.2	60.0	34	5	US-09-536-784-316
c 14	12.2	60.0	34	6	US-09-765-272-316
c 15	11.8	59.0	37	7	US-09-591-306-33
c 16	11.6	58.0	18	8	US-60-301-889-40
c 17	11.6	58.0	26	5	US-09-310-735A-328
c 18	11.6	58.0	26	5	US-09-310-735A-346
c 19	11.6	58.0	26	5	US-09-310-844B-328
c 20	11.6	58.0	26	5	US-09-310-844B-346
c 21	11.6	58.0	40	7	US-60-301-889-41
c 22	11.6	58.0	42	7	US-09-840-424-747
c 23	11.6	58.0	48	5	US-09-554-941-5
c 24	11.6	58.0	50	8	US-60-252-833-36224
c 25	11.6	58.0	50	8	US-60-253-456-6918

c 26 11.4 57.0 25 6 US-09-907-574-15 Sequence 15, Appl  
27 11.2 56.0 17 6 US-09-546-745A-1852 Sequence 1852, Ap  
28 11.2 56.0 17 6 US-09-546-745A-1853 Sequence 1853, Ap  
c 29 11.2 56.0 17 6 US-09-817-879-2491 Sequence 2491, Ap  
c 30 11.2 56.0 20 7 US-09-920-759-70 Sequence 70, Appl  
31 11.2 56.0 23 6 US-09-375-318-66 Sequence 66, Appl  
32 11.2 56.0 24 6 US-09-465-589-6 Sequence 6, Appl  
c 33 11.2 56.0 24 6 US-09-465-589-6 Sequence 6, Appl  
c 34 11.2 56.0 30 6 US-09-535-370-118 Sequence 118, App  
c 35 11.2 56.0 30 6 US-09-139-031C-35 Sequence 35, Appl  
c 36 11.2 56.0 30 7 US-09-898-541-18 Sequence 18, Appl  
37 11.2 56.0 31 5 US-09-574-376B-787 Sequence 787, App  
38 11.2 56.0 31 6 US-09-801-274-1514 Sequence 1514, Ap  
c 39 11.2 56.0 32 6 US-09-465-589-15 Sequence 15, Appl  
c 40 11.2 56.0 32 6 US-09-465-589-15 Sequence 15, Appl  
c 41 11.2 56.0 39 8 US-60-253-456-28591 Sequence 28591, A  
42 11.2 56.0 50 6 US-09-684-610B-345 Sequence 345, App  
43 11 55.0 25 7 US-09-804-661-4 Sequence 4, Appl  
c 44 11 55.0 27 5 US-09-837-235-39 Sequence 39, Appl  
45 11 55.0 27 5 US-09-837-235-40 Sequence 40, Appl

#### ALIGNMENTS

RESULT 1  
US-09-715-849-159/c  
; Sequence 159, Application US/09715849  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: 2825.2002-001  
; CURRENT APPLICATION NUMBER: US/09/715.849  
; CURRENT FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/167,334  
; PRIOR FILING DATE: 1999-11-24  
; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 159  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-715-849-159

Query Match 64.0%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 77.8%; Pred. No. 4.3e+03;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagctt 18  
||| ||| : |||||  
Db 18 CATAATTYTAAGCTT 1

RESULT 2  
US-09-536-784-418/c  
; Sequence 418, Application US/09536784  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
ADDRESS: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33

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;
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 418:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 418:
US-09-536-784-418

Query Match 63.0%; Score 12.6; DB 5; Length 36;
Best Local Similarity 78.9%; Pred. No. 5.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 atgagtcttaaaagcttac 20
   || || | | | |||||
Db 21 ATTATGTTGATAAGCTTAC 3

RESULT 3
US-09-765-272-418/c
; Sequence 418, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 418:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
```

```
;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 418:
US-09-765-272-418

Query Match 63.0%; Score 12.6; DB 6; Length 36;
Best Local Similarity 78.9%; Pred. No. 5.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 atgagtcttaaaagcttac 20
   || || | | | |||||
Db 21 ATTATGTTGATAAGCTTAC 3

RESULT 4
US-09-536-784-330/c
; Sequence 330, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 330:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 330:
US-09-536-784-330

Query Match 61.0%; Score 12.2; DB 5; Length 33;
Best Local Similarity 82.4%; Pred. No. 9.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 gatgcttaaaagcttac 20
   || || | | | |||||
Db 19 GAAGCTAATAAGCTTAC 3

RESULT 5
US-09-765-272-330/c
; Sequence 330, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
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```

CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765.272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 330:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 330:
US-09-765-272-330

```

Query Match 61.0%; Score 12.2; DB 6; Length 33;  
Best Local Similarity 82.4%; Pred. No. 9.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels

Oy 4 gatgcttaaagcttac 20  
|||  
Db 19 GAAGCTAATAAGCTTAC 3

```

RESULT      6
US-60-253-378-31544
; Sequence 31544, Application US/60253378
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides isolated from plants
; TITLE OF INVENTION: and methods for their use.
; FILE REFERENCE: 1054p3
; CURRENT APPLICATION NUMBER: US/60/253,378
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 40367
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31544
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-378-31544

```

Query Match 61.0%; Score 12.2; DB 8; Length 41;  
Best Local Similarity 82.4%; Pred. No. 9.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels

Qy 2 atgatgcttaaagctt 18  
||||| ||||| |||  
Db 15 atgattcttaaacgcat 31

```

RESULT      7
US-60-295-722-6/c
; Sequence 6, Application US/60295722
; GENERAL INFORMATION:
; APPLICANT: Barbara Bour
; APPLICANT: John Chicca
; APPLICANT: Blake Denison
; APPLICANT: Frances Yen
; APPLICANT: Bernard Bihain
; APPLICANT: Lydie Bougueleret
; TITLE OF INVENTION: GSSP4 Polynucleotides and Polypeptides and Uses Thereof
; FILE REFERENCE: 103.US2.PRO
; CURRENT APPLICATION NUMBER: US/60/295,722
; PRIOR FILING DATE: 2001-06-04
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-295-722-6

```

Query Match	61.0%	Score 12.2;	DB 8;	Length 47;
Best Local Similarity	82.4%;	Pred. No. 9.6e+03;		
Matches 14;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy 4 gatgcttaaaagcttac 20  
||| ||| ||| ||| |||  
Db 23 GAAGTTTATAAGCTTAC 7

```

RESULT      8
US-60-295-600-6/c
; Sequence 6, Application US/60295600
; GENERAL INFORMATION:
; APPLICANT: Barbara Bour
; APPLICANT: John Chicca
; APPLICANT: Blake Dentson
; APPLICANT: Frances Yen
; APPLICANT: Bernard Bhain
; APPLICANT: Lydie Bouqueteret
; TITLE OF INVENTION: GSP4 Polynucle
; FILE REFERENCE: 104.US2.PRO
; CURRENT APPLICATION NUMBER: US/60-
; CURRENT FILING DATE: 2001-06-04
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-295-600-6

```

Query Match	61.0%	Score 12.2;	DB 8;	Length 47;
Best Local Similarity	82.4%;	Pred. No. 9.6e+03;		
Matches 14;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy 4 gatgcttaaagcttac 20  
|||  
Db 23 GAAGTTTATAAGCTTAC 7

RESULT 9  
US-60-295-722-6/c  
; Sequence 6, Application US/60295722  
; GENERAL INFORMATION:  
; APPLICANT: Barbara Bour  
; APPLICANT: John Chicca

APPLICANT: Blake Denison  
APPLICANT: Frances Yen  
APPLICANT: Bernard Bihain  
APPLICANT: Lydie Bouquellet  
TITLE OF INVENTION: GSP4 Polynucleotides and Polypeptides and Uses Thereof  
FILE REFERENCE: 103.052.PRO  
CURRENT APPLICATION NUMBER: US/60/295,722  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patent.pm  
SEQ ID NO 6  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-295-722-6

Query Match 61.0%; Score 12.2; DB 8; Length 47;  
Best Local Similarity 82.4%; Pred. No. 9.6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 4 gatgcttaaaagcttac 20  
Db 23 GAAGTTTATAAGCTTAC 7

RESULT 10  
US-09-923-515-39  
Sequence 39, Application US/09923515  
GENERAL INFORMATION:  
APPLICANT: Rosanne M. Crooke  
APPLICANT: Mark J. Graham  
TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN(A) EXPRESSION  
FILE REFERENCE: ISPH-0595  
CURRENT APPLICATION NUMBER: US/09/923,515  
CURRENT FILING DATE: 2001-08-07  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 39  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-923-515-39

Query Match 60.0%; Score 12; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 cttaaaagctta 19  
Db 3 cttaaaagctta 14

RESULT 11  
US-09-536-784-272/c  
Sequence 272, Application US/09536784  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/536,784  
FILING DATE: 30-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: OCT-30-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB340P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 272:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 272:  
US-09-536-784-272

Query Match 60.0%; Score 12; DB 5; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20  
Db 22 CATACTGCAGATAAGCTTAC 3

RESULT 12  
US-09-765-272-272/c  
Sequence 272, Application US/09765272  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,272  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 272:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

```
;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-765-272-272

Query Match          60.0%; Score 12; DB 6; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20
   ||| ||| | |||||
Db 22 CACTAGCAGATAAGCTTAC 3

RESULT 13
US-09-536-784-316/c
; Sequence 316, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340p3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 316:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 316:
US-09-536-784-316

Query Match          60.0%; Score 12; DB 5; Length 34;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20
   ||| ||| | |||||
Db 22 CACTAGCAGATAAGCTTAC 3

RESULT 14
US-09-765-272-316/c
; Sequence 316, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340p2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 316:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 316:
US-09-765-272-316

Query Match          60.0%; Score 12; DB 6; Length 34;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20
   ||| ||| | |||||
Db 22 CCTACTGATTATAAGCTTAC 3

RESULT 15
US-09-591-306-33
; Sequence 33, Application US/09591306
; GENERAL INFORMATION:
; APPLICANT: Massachusetts general Hospital
; TITLE OF INVENTION: Novel transcription factor and uses therefor
; FILE REFERENCE: 17633/1170
; CURRENT APPLICATION NUMBER: US/09/591,306
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 08/751,344
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(37)
; OTHER INFORMATION: Synthetic primer
US-09-591-306-33

Query Match          59.0%; Score 11.8; DB 7; Length 37;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 atgatgcttaaaagc 16  
||| ||| |||||  
Db 15 atggtgcgtataaagc 29

Search completed: October 2, 2001, 16:55:06  
Job time: 17669 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:46 ; Search time 876.95 seconds

(without alignments)  
10.740 Million cell updates/sec

Title: US-09-757-100B-23

Perfect score: 15

Sequence: 1 gcgggctcacagtgg 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0601.\*  
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2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
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6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
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19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	Human focal adhesi
2	15	100.0	20	22	Human focal adhesi
c 3	13.4	89.3	31	22	Oligonucleotide sf
c 4	11.8	78.7	20	19	Human NKCC2 gene e
5	11.8	78.7	24	20	PCR primer used to
6	11.8	78.7	31	18	Primer murF2. Syn
7	11.8	78.7	31	19	3' PCR primer used
8	11.8	78.7	31	20	PCR primer used to
9	11.8	78.7	39	11	Oligonucleotide ca
10	11.8	78.7	39	18	Primer murF4. Syn
11	11.8	78.7	39	20	PCR primer used to

12	11.8	78.7	44	21	AAA72106	HIV-1 gp41 C-helic
13	11.8	78.7	47	20	AAZ01125	probe for human PG
c 14	11.4	76.0	18	22	AAF94736	Rho G antisense ph
c 15	11.4	76.0	22	18	AA45334	Mycoplasma second
16	11.4	76.0	29	21	AA04346	Polymorphic fragme
c 17	11.4	76.0	45	21	AA01093	PCR primer ZC17157
18	11.4	76.0	48	20	AAAX26801	Primer for 564/5/6
c 19	11.1	73.3	21	20	AAAX88971	Mouse vascular end
c 20	11	73.3	31	14	AA040032	Sequence of forwar
c 21	11	73.3	31	16	AA089636	Forward primer 34F
c 22	10.8	72.0	15	22	AAAF52005	IGF-I oligonucleot
c 23	10.8	72.0	15	22	AAAF52006	IGF-I oligonucleot
c 24	10.8	72.0	17	18	AAAG2250	Granule bound star
25	10.8	72.0	18	20	AAAZ30563	Human integrin alp
26	10.8	72.0	20	19	AAV18312	Measles virus L pr
27	10.8	72.0	20	20	AAZ22946	Primer specific fo
28	10.8	72.0	21	21	AAAG5140	Primer #3 targeted
c 29	10.8	72.0	24	16	AAAT03859	Primer BLGAMP4 for
30	10.8	72.0	24	17	AAAT31052	Human fibroblast g
c 31	10.8	72.0	24	18	AAAT79727	Beta-lactoglobulin
32	10.8	72.0	24	20	AAAX00053	Human FGFRI-PI PCR
c 33	10.8	72.0	24	21	AAAG5581	Murine proteinase
c 34	10.8	72.0	29	14	AAQ50767	ERM HIV target seq
c 35	10.8	72.0	29	16	AAQ83139	HIVPCV12 No. 1960
c 36	10.8	72.0	30	13	AAQ25250	NANBH PCR primer P
37	10.8	72.0	30	22	AAQ02858	Human GPVI externa
38	10.8	72.0	32	14	AAQ47793	Billirubin oxidase
c 39	10.8	72.0	32	22	AAAC92387	CD100 PCR primer S
40	10.8	72.0	36	21	AAZ57915	Escherichia coli t
41	10.8	72.0	40	21	AAZ55715	Anabaena variabill
42	10.8	72.0	50	21	AAZ47143	Liposome membrane
43	10.6	70.7	31	20	AAAX38989	Human genomic DNA
44	10.4	69.3	17	20	AAV92548	Human A-Raf substr
c 45	10.4	69.3	20	22	AAAF92436	Human CYP3A relate

#### ALIGNMENTS

RESULT 1  
AAC65555  
ID AAC65555 standard; DNA; 15 BP.  
XX  
AC AAC65555;  
XX  
XX  
DT 12-FEB-2001 (first entry)  
XX  
XX Human focal adhesion kinase antisense sequence #21.  
DE  
XX Human; focal adhesion kinase; FAK; signal transduction; cancer;  
KW embryonic development disorder; angiogenic disorder; wound healing;  
KW antisense; phosphothioate; ss.  
XX  
OS Homo sapiens.  
XX  
XX US6133031-A.  
XX  
XX 17-OCT-2000.  
XX  
XX 19-AUG-1999; 99US-0377310.  
XX  
XX 19-AUG-1999; 99US-0377310.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Monia BP, Gaarde WA;  
XX  
XX WPI; 2001-006141/01.  
XX  
XX New antisense compounds for inhibiting focal adhesion kinase  
PT expression, especially useful for inhibiting retinal  
PT neovascularization, or for diagnosing and treating e.g. colon cancer -  
XX

PS Claim 3; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
is involved in integrin-mediated signal transduction, and is implicated  
CC in cancer, particularly colon, breast and oral tumours, embryonic  
CC development disorders, angiogenic disorders and wound healing. The  
CC antisense sequences, including the one shown here, can be used in the  
XX treatment of all of these.

SQ Sequence 15 BP; 2 A; 4 C; 7 G; 2 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 22;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15  
Db 1 gcgggctcacagtgg 15  
|||||

RESULT 2

AAC65535  
ID AAC65535 standard; DNA; 20 BP.

XX AAC65535;

DT 12-FEB-2001 (first entry)

DE Human focal adhesion kinase antisense sequence #1.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;  
KW embryonic development disorder; angiogenic disorder; wound healing;  
KW antisense; phosphorothioate; ss.

XX Homo sapiens.

PN US613031-A.

PD 17-OCT-2000.

PF 19-AUG-1999; 99US-0377310.

PR 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

PI Monia BP, Gaarde WA;

DR WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase  
PT expression, especially useful for inhibiting retinal  
PT neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Claim 3; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
is involved in integrin-mediated signal transduction, and is implicated  
CC in cancer, particularly colon, breast and oral tumours, embryonic  
CC development disorders, angiogenic disorders and wound healing. The  
CC antisense sequences, including the one shown here, can be used in the  
XX treatment of all of these.

SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 15; DB 22; Length 20;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15  
Db 3 gcgggctcacagtgg 17  
|||||

RESULT 3  
AAC83406/c  
ID AAC83406 standard; DNA; 31 BP.

XX AAC83406;

DT 26-FEB-2001 (first entry)

DE Oligonucleotide sfAZ2.

KW Translational reporter vector; renilla luciferase;

KW translational recoding; ss.

XX Synthetic.

PN US6143502-A.

PD 07-NOV-2000.

PF 31-MAR-1999; 99US-0282996.

PR 31-MAR-1999; 99US-0282996.

XX (UTAH) UNIV UTAH RES FOUND.

PI Grentzmann G, Atkins JF, Gesteland RF;

DR WPI; 2001-006431/01.

PT Translational reporter vector for quantification of translation

PT recoding in vivo and in vitro, comprises renilla luciferase gene,

PT polylinker for insertion of selected DNA and an out-of-frame firefly

PT luciferase gene -

PS Example 4; Column 33; 21pp; English.

XX The present invention relates to a translational reporter vector  
CC selected from p2luc and p2luc1. The vectors have a polylinker  
CC interposed between a renilla luciferase gene and a firefly luciferase  
CC gene, which are out-of-frame with respect to each other but are  
CC co-expressed upon recoding. The translational reporter vector is  
CC useful for assaying translational recoding in vitro or in vivo.

SQ Sequence 31 BP; 4 A; 10 C; 9 G; 8 T; 0 other;

Query Match 89.3%; Score 13.4; DB 22; Length 31;

Best Local Similarity 93.3%; Pred. No. 1.7e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15  
Db 23 GCGGGATCACAGTGG 9  
|||||

RESULT 4

AAV45725/c

ID AAV45725 standard; DNA; 20 BP.

XX AAV45725;

DT 21-DEC-1998 (first entry)

DE Human NKCC2 gene exon 24 forward primer hNKCC2ex24.

KW Na-K-2Cl cotransporter; NKCC2; human; Bartter's syndrome;

KW nephrocalcinosis; hypokalaemic alkalosis; hypercalciuria;

KW nephrocalcinosis; diagnosis; therapy; SSCP; primer; ss.

XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN WO9829431-A1.  
 XX PN 09-JUL-1998.  
 XX PF 19-DEC-1997; 97WO-US23553.  
 XX PR 31-DEC-1996; 96US-0778052.  
 XX PA (UYIA ) UNIV YALE.  
 XX PI Lifton RP, Simon DB;  
 XX DR WPI; 1998-388029/33.  
 XX PT Thiazide sensitive cotransporter, ATP sensitive K channel and NaK2Cl cotransporter genes - useful for developing products for the diagnosis and treatment of ion transport disorders, e.g. Gitelman's Syndrome or Bartter's Syndrome  
 XX PS Example 2; Page 65; 105pp; English.  
 XX CC Primers hNKCC2ex24 forward and reverse (see AAV45725 and AAV45726, respectively) are designed to amplify exon 24 of the human NKCC2 gene (see AAV40562) that codes for Na-K-2Cl cotransporter NKCC2 protein (see AAV29683). Both primers are located within introns of the gene. 27 Sets of specific primers (see AAV45677-V45730) were used for SSCP analysis of NKCC2. Amplified products were analysed for molecular variants by electrophoresis, and identified variants were sequenced. Complete linkage of Bartter's syndrome with NKCC2 was demonstrated. Identification of the molecular basis of Bartter's syndrome allows for the genetic diagnosis of this disorder. The invention provides products and methods useful for diagnosis and treatment of Bartter's syndrome and other ion transport disorders.  
 XX SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 other;

Query Match 78.7%; Score 11.8; DB 19; Length 20;  
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 gcggggtcacagtgg 15  
 ||| |||||  
 DB 20 GAGGCTCACAGTGG 6

RESULT 5  
 AAX36171  
 ID AAX36171 standard; DNA; 24 BP.  
 XX AC  
 XX AAX36171;  
 XX DT 15-JUL-1999 (first entry)  
 XX DE PCR primer used to amplify a fragment of ICAM-6 nucleic acid.  
 XX KW Intercellular adhesion molecule 6; ICAM-6; drug screening; therapy;  
 XX KW Intercellular adhesion; inflammatory process; PCR primer; ss.  
 XX OS Synthetic.  
 XX PN WO9920762-A1.  
 XX PD 29-APR-1999.  
 XX PF 22-OCT-1998; 98WO-US22442.  
 XX PR 22-OCT-1997; 97US-0955661.

XX PA (ICOS-) ICOS CORP.  
 XX PI Loughney K, Staunton DE, Vazeau R;  
 XX DR WPI; 1999-288308/24.  
 XX PT New isolated intercellular adhesion molecule-6 used for, e.g. diagnosis of inflammatory processes  
 XX PS Example 15; Page 53; 102pp; English.  
 XX CC The specification describes an intercellular adhesion molecule (ICAM)-6 polypeptide. The ICAM-6 polypeptides and polynucleotides can be used for drug screening and developing products for therapy involving intercellular adhesion, e.g. in inflammatory processes. The products can also be used for detection, diagnosis and the production of transgenic animals. PCR primers AAX36170-73 were used in the course of the invention.  
 XX SQ Sequence 24 BP; 6 A; 3 C; 10 G; 5 T; 0 other;

Query Match 78.7%; Score 11.8; DB 20; Length 24;  
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 gcggggtcacagtgg 15  
 ||| |||||  
 DB 10 gctggatcacagtgg 24

RESULT 6  
 AAT63364  
 ID AAT63364 standard; DNA; 31 BP.  
 XX AC AAT63364;  
 XX DT 07-SEP-1997 (first entry)  
 XX DE Primer murF2.  
 XX KW Recombinant plasmid; DNA immunisation; genetic vaccine; gene therapy; murF gene; Escherichia coli; primer; PCR;  
 XX KW polymerase chain reaction; ss.  
 XX OS Synthetic.  
 XX PN WO9714805-A2.  
 XX PD 24-APR-1997.  
 XX PF 17-OCT-1996; 96WO-CA00693.  
 XX PR 30-NOV-1995; 95US-0564973.  
 XX PR 17-OCT-1995; 95US-0548059.  
 XX PA (BIOS-) BIOTAR INC.  
 XX PI Morsey MA;  
 XX DR WPI; 1997-245120/22.  
 XX PT Culture system for stable high yield production of recombinant plasmids - using bacteria with modified chromosome that can survive only when plasmid is present and optionally foreign DNA expressible only in eukaryote(s)  
 XX PS Example 1; Page 20; 46pp; English.  
 XX CC Primers murF1 (AAT63363) and murF2 (AAT63364) were used to amplify the Escherichia coli murF gene (see also AAT63360) and were designed so as to allow in-frame fusion of the murF coding sequence to the

CC murE promoter. The murE promoter was subsequently amplified (see  
 CC also AAF63365-66). An E. coli strain was constructed with an  
 CC irreversible alteration (deletion) in its murF gene. This can  
 CC be used for large-scale prodn. of recombinant plasmids.  
 XX

SQ Sequence 31 BP; 6 A; 9 C; 13 G; 3 T; 0 other;

Query Match 78.7%; Score 11.8; DB 18; Length 31;  
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15  
 || |||| |||||  
 Db 12 gcaggctgacagtgg 26

RESULT 7  
 AAV42721  
 ID AAV42721 standard; DNA; 31 BP.  
 AC AAV42721;  
 XX  
 XX  
 DT 14-OCT-1998 (first entry)  
 DE 3' PCR primer used to amplify human furin cDNA.  
 XX  
 XX  
 KW Retroviral vector; gene delivery vehicle; expression; PCR primer;  
 KW non-immunogenic selectable marker; gene therapy; activation;  
 KW human; furin; ablation therapy; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9830709-A2.  
 PN  
 XX  
 PD 16-JUL-1998.  
 PF 14-JAN-1998; 98WO-US00715.  
 XX  
 XX 13-JAN-1998; 98US-0038339.  
 PR 14-JAN-1997; 97US-0038473.  
 PR 27-FEB-1997; 97US-0038339.  
 XX

XX (CHAD/) CHADA S.  
 PA (JOLLY/) JOLLY D J.  
 PA (MOOR/) MOORE M D.  
 XX  
 PI Chada S, Jolly DJ, Moore MD;  
 DR WPI; 1998-399153/34.  
 XX  
 PT Non-immunogenic pro-drug activating enzyme(s) and selectable  
 PT marker(s) are used in gene therapy for the treatment of a wide  
 PT variety of disorder(s)  
 XX  
 PS Example 8; Page 53; 121pp; English.  
 XX  
 CC PCR primers AAV42720-21 were used to amplify human furin cDNA (see  
 CC AAV42731). The amplified product is used in the retroviral vector of the  
 CC invention to encode a cell bound prodrug convertase for ablation therapy.  
 CC The specification describes a gene delivery vehicle which directs  
 CC expression of a non-immunogenic selectable marker or molecule which is  
 CC capable of activating a previously inactive compound. Vectors expressing  
 CC the markers and a heterologous sequence are useful in gene therapy. The  
 CC vectors can be used to deliver a molecule into a target area where it may  
 CC cause the activation of a previously inactive substance.  
 XX  
 SQ Sequence 31 BP; 5 A; 12 C; 10 G; 4 T; 0 other;

Query Match 78.7%; Score 11.8; DB 19; Length 31;  
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 gcgggctcacagtgg 15  
 || |||| |||||  
 Db 13 gtgggctcacaggg 27

RESULT 8  
 AAX86099  
 ID AAX86099 standard; DNA; 31 BP.  
 XX  
 AC AAX86099;  
 XX  
 DT 13-SEP-1999 (first entry)  
 DE PCR primer used to amplify the murF gene.  
 XX

KW Culture system; high level production; recombinant plasmid; murF;  
 KW plasmid replication; plasmid production; DNA immunisation; gene therapy;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US5922583-A.  
 PN  
 XX 13-JUL-1999.  
 PD  
 XX 16-OCT-1996; 96US-0732612.  
 PF  
 XX 16-OCT-1996; 96US-0732612.  
 PR  
 PR 17-OCT-1995; 95US-0548059.  
 PR 30-NOV-1995; 95US-0564973.  
 XX  
 XX (BIOS-) BIOSTAR INC.  
 PA  
 XX  
 PI Morsey MA;  
 XX  
 XX WPI; 1999-404463/34.  
 XX

PT Culture system for stable and high-level production of DNA contained  
 PT on recombinant plasmids, with improved plasmid stability  
 XX  
 PS Example 1; Column 13; 27pp; English.  
 XX  
 CC The specification describes a culture system for stable high-level  
 CC production of recombinant plasmids. The method comprises propagating  
 CC irreversibly altered bacterial cells under conditions such that cell  
 CC viability is dependent on the recombinant plasmid. The system is used  
 CC is for the replication and high-level production of structurally and  
 CC genetically stable recombinant plasmids carrying DNA, this DNA can  
 CC then be used in DNA immunisation or gene therapy. PCR primers  
 CC AAX86098-99 were used to amplify the murF gene, for use in the method  
 CC of the invention.  
 XX  
 SQ Sequence 31 BP; 6 A; 9 C; 13 G; 3 T; 0 other;

Query Match 78.7%; Score 11.8; DB 20; Length 31;  
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15  
 || |||| |||||  
 Db 12 gcaggctgacagtgg 26

RESULT 9  
 AAQ04938  
 ID AAQ04938 standard; DNA; 39 BP.  
 XX  
 AC AAQ04938;  
 XX  
 DT 24-OCT-1990 (first entry)

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XX DE Oligonucleotide carrying mutation for factor VIII gene.
XX KW Human factor VIII analogue; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT mutation 18..23
XX FT /*tag= a
XX PN WO9005530-A.
XX PD 31-MAY-1990.
XX PF 14-NOV-1989; 89WO-0005049.
XX PR 14-NOV-1988; 88US-0270882.
XX PA (GENE-) GENETICS INST INC.
XX PI Kaufman RJ, Pittman DD;
XX DR WPI; 1990-193265/25.
XX DE New hybrid DNA encoding hybrid procoagulant proteins -
XX FT prepd. by modifying DNA encoding human factor VIII.
XX PS Disclosure; ; pp: English.
XX CC Factor VIII analogue is sufficiently mutated from the original gene
XX CC that it is not recognised by blood Abs of the patient. The analogue
XX CC is composed of human FVIII but carries the B-domain of human FV in
XX CC place of the FVIII B-domain.
XX CC Oligonucleotides can be used to alter the profile of the blood
XX CC factor without significantly altering its activity.
XX SQ Sequence 39 BP; 9 A; 11 C; 11 G; 8 T; 0 other;

Query Match 78.7%; Score 11.8; DB 11; Length 39;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
Db ||| ||||| |||||

RESULT 10
AAT63369
ID AAT63369 standard; DNA; 39 BP.
XX AC AAT63369;
XX DT 07-SEP-1997 (first entry)
XX DE Primer murF4.
XX KW Recombinant plasmid; DNA immunisation; genetic vaccine;
XX KW gene therapy; murF gene; Escherichia coli; primer; PCR;
XX KW polymerase chain reaction; ss.
XX OS Synthetic.
XX PN WO9714805-A2.
XX PD 24-APR-1997.
XX PF 17-OCT-1996; 96WO-CA00693.
XX PR 30-NOV-1995; 95US-0564973.
XX PR 17-OCT-1995; 95US-0548059.

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XX PA (BIOS-) BIOSTAR INC.
XX PI Morsey MA;
XX DR WPI; 1997-245120/22.
XX PT Culture system for stable high yield production of recombinant
XX PT plasmids - using bacteria with modified chromosome that can survive
XX PT only when plasmid is present and optionally foreign DNA expressible
XX PS only in eukaryote(s)
XX PS Example 2; Page 23; 46pp; English.
XX CC Primers murF3 (AAT63368) and murF4 (AAT63369) were used to amplify the
XX CC temperature-sensitive murF gene (see also AAT63360) from Escherichia
XX CC coli TKL-68. The amplified nucleotide sequence was cloned into
XX CC the BamHI site of pUC19, and can be used to produce temperature-
XX CC sensitive bacterial host cells useful for large-scale prodn. of
XX CC recombinant plasmids.
XX SQ Sequence 39 BP; 9 A; 10 C; 15 G; 5 T; 0 other;

Query Match 78.7%; Score 11.8; DB 18; Length 39;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
Db ||| ||||| |||||

RESULT 11
AAX86104
ID AAX86104 standard; DNA; 39 BP.
XX AC AAX86104;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify the murF gene.
XX KW Culture system; high level production; recombinant plasmid; murF;
XX KW plasmid replication; plasmid production; DNA immunisation; gene therapy;
XX KW PCR primer; ss.
XX OS Synthetic.
XX PN US922583-A.
XX PD 13-JUL-1999.
XX PF 16-OCT-1996; 96US-0732612.
XX PR 16-OCT-1996; 96US-0732612.
XX PR 17-OCT-1995; 95US-0548059.
XX PR 30-NOV-1995; 95US-0564973.
XX PA (BIOS-) BIOSTAR INC.
XX PI Morsey MA;
XX DR WPI; 1999-404463/34.
XX CC Culture system for stable and high-level production of DNA contained
XX CC on recombinant plasmids, with improved plasmid stability
XX PS Example 2; Column 15; 27pp; English.
XX CC The specification describes a culture system for stable high-level
XX CC production of recombinant plasmids. The method comprises propagating
XX CC irreversibly altered bacterial cells under conditions such that cell

```

CC viability is dependent on the recombinant plasmid. The system is used  
 CC is for the replication and high-level production of structurally and  
 CC genetically stable recombinant plasmids carrying DNA, this DNA can  
 CC then be used in DNA immunisation or gene therapy, PCR primers  
 CC AAX86102-03 were used to amplify the murf gene, for use in the method  
 CC of the invention.

XX Sequence 39 BP; 9 A; 10 C; 15 G; 5 T; 0 other;

Query Match 78.7%; Score 11.8; DB 20; Length 39;  
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15  
 || |||| |||||  
 Db 20 gcaggctgacagtgg 34

## RESULT 12

AAA72106  
 ID AAA72106 standard; DNA; 44 BP.

XX AC AAA72106;

XX DT 24-NOV-2000 (first entry)

XX DE HIV-1 gp41 C-helical domain 5' PCR primer.

XX KW HIV-1; gp41; N-helical domain; heptad repeat region; C-helical domain;  
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KW core 6-helix bundle; viral entry inhibition; immunogenic;  
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KW envelope glycoprotein; prophylaxis; therapy; PCR primer; ss.

XX OS Human Immunodeficiency virus type 1.

XX PN WO200040616-A1.

XX PD 13-JUL-2000.

XX PF 10-JAN-2000; 2000WO-US00456.

XX PR 08-JAN-1999; 99US-0115404.

XX PR 07-JAN-2000; 2000US-0480336.

XX PA (WILD/) WILD C. T.

XX PA (WEIS/) WEISS C. D.

XX PI Wild CT, Weiss CD;

XX DR WPI; 2000-465959/40.

PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure.

XX Example 5; Page 54; 97pp; English.

XX The invention relates to raising a neutralising antibody response to a  
 CC broad spectrum of HIV (human immunodeficiency virus) strains and  
 CC isolates, comprising the administration of a peptide which corresponds  
 CC to or mimics highly conserved portions of the gp41 envelope glycoprotein  
 CC which are important in mediating the process of viral entry into host  
 CC cells. Such peptides can correspond to or mimic the coiled coil  
 CC solution structure of the N-helical domain (the heptad repeat  
 CC region), or can correspond or mimic the C-helical domain (the  
 CC transmembrane-proximal amphipathic alpha-helical segment), or the  
 CC gp41 core 6-helix bundle, which is formed by the interaction of  
 CC the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly  
 CC a combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can be

CC alternately linked together to form a peptide which mimics the core  
 CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
 CC response, with the production of antibodies against gp41 structures  
 CC involved in viral entry. As these portions of gp41 are well conserved,  
 CC such antibodies may be effective against a broad range of HIV strains  
 CC and isolates. The peptide compositions may be administered as a  
 CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
 CC or inhibit the ability of HIV to infect uninfected cells. A composition  
 CC comprising polyclonal or monoclonal antibodies can be administered to  
 CC reduce HIV infection of uninfected cells. Antibodies raised against  
 CC entry-relevant gp41 structures may also be used therapeutically and as  
 CC tools to further elucidate the mechanism of HIV cell entry.  
 CC Sequences AAA72104-A72107 represent PCR primers used in an  
 CC exemplification of the invention to construct DNA (AAA72102) encoding a  
 CC protein construct (AAB14603) comprising the N- and C-helical domains of  
 CC HIV-1 gp41 separated by a short peptide linker.

XX SQ Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 other;

Query Match 78.7%; Score 11.8; DB 21; Length 44;  
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15  
 || |||| |||||  
 Db 9 gccggctcagagtgg 23

## RESULT 13

AAZ01125

ID AAZ01125 standard; DNA; 47 BP.

XX AC AAZ01125;

XX DT 27-SEP-1999 (first entry)

XX DE Probe for human PGI biallelic marker 4-50-293.

XX KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;  
 KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;  
 KW PSA; human; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9932644-A2.

XX PD 01-JUL-1999.

XX PF 22-DEC-1998; 98WO-IB02133.

XX PR 09-SEP-1998; 98US-0099658.

XX PR 22-DEC-1997; 97US-0996306.

XX PA (GEST ) GENSET.

XX PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;

XX DR WPI; 1999-405178/34.

PT Use of a prostate cancer associated gene and biallelic markers  
 PT derived from it

XX Claim 4; Page 328; 385pp; English.

XX The invention relates to a mammalian PGI gene and protein, and a set of  
 CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are  
 CC used in a hybridisation assay, a sequencing assay, or in an  
 CC allele-specific amplification assay for determining the identity of a  
 CC nucleotide at a PGI-related biallelic marker. The methods can be used to  
 CC detect and to assess the risk of developing cancer or prostate cancer.  
 CC Early-stage diagnosis of prostate cancer relies on prostate specific

CC antigen (PSA) dosage. However, the effectiveness of this is limited due  
CC to its inability to discriminate between malignant and non-malignant  
CC affections of the organ. A need exists for both a reliable diagnostic  
CC procedure which would enable early-stage diagnosis, and for preventative  
CC and curative treatments of the disease. The PGI gene can be used for  
CC detection of prostate cancer, and the risk of developing it in the  
CC future, and can also be used to determine therapies for the disease.  
XX  
SQ Sequence 47 BP; 14 A; 9 C; 14 G; 10 T; 0 other;

Query Match 78.7%; Score 11.8; DB 20; Length 47;  
Best Local Similarity 86.7%; Pred. No. 1.3e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 qcgggctcacagtgg 15  
| | | | | | | | | | |  
Db 12 gggggctgacagtgg 26

RESULT 14  
AAF94736/c  
ID AAF94736 standard; DNA; 18 BP.

XX AAF94736;

AC AAF94736;

XX 23-MAY-2001 (first entry)

DE Rho G antisense phosphorothioate oligonucleotide SEQ ID 160.

XX Rho; GTP binding protein; phosphorothioate antisense oligonucleotide;  
KW RhoA; RhoB; RhoC; RhoG; Rac 1; cdc42; hyperproliferative condition;  
KW cancer; wound healing; clotting; ischaemia; reperfusion; reoxygenation;  
KW ss.

XX Homo sapiens.

OS

XX WO200115739-A1.

PN 08-MAR-2001.

PD 18-AUG-2000; 2000WO-US22808.

PF 31-AUG-1999; 99US-0387341.

XX (ISIS-) ISIS PHARM INC.

XX Roberts ML, Cowsert LM;

XX WPI; 2001-191677/19.

XX An antisense compound targeted to a nucleic acid molecule encoding a

PT member of the human Rho family of small GTP binding proteins useful for

PT treating e.g. cancer and ischaemia -

XX Example 18; Page 81; 156pp; English.

XX This invention relates to an antisense compound targeted to a nucleic  
CC acid molecule encoding a member of the human Rho family of small GTP  
CC binding proteins, where the antisense compound inhibits the expression of  
CC the member of the human Rho family. The invention includes antisense  
CC oligonucleotides AAF94580 - AAF94637 which target a RhoA nucleotide  
CC sequence, AAF94645 - AAF94684 which target a RhoB nucleotide sequence,  
CC AAF94686 - AAF94725 which target a RhoC nucleotide sequence, AAF94727 -  
CC AAF94766 which target RhoG nucleotide sequence, AAF94769 - AAF94790 which  
CC target a Rac 1 nucleotide sequence and AAF94795 - AAF94809 which target  
CC cdc42 nucleotide sequence. The antisense compound is useful for treating  
CC hyperproliferative conditions, especially cancer, abnormal wound healing  
CC or clotting conditions and ischaemia/reperfusion or reoxygenation injury.  
CC The compound may also be used to diagnose the above conditions.

XX Sequence 18 BP; 1 A; 6 C; 6 G; 5 T; 0 other;

Query Match 76.0%; Score 11.4; DB 22; Length 18;  
Best Local Similarity 92.3%; Pred. No. 2e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 14  
| | | | | | | | | | |  
Db 17 CGGGCGCACAGTG 5

RESULT 15  
AAT45334/c  
ID AAT45334 standard; DNA; 22 BP.

XX AAT45334;

AC AAT45334;

XX 10-JUL-1997 (first entry)

DE Mycoplasma second stage PCR primer M34.

XX Polymerase chain reaction; Mycoplasma; M.fermentans; M.hyorhinis;  
KW M.arginini; M.pirum; M.hominis; M.salivarium; M. orale; detection; ss.

XX Synthetic.

XX WO9636735-A1.

XX 21-NOV-1996.

XX 13-MAY-1996; 96WO-US07116.

XX 19-MAY-1995; 95US-0445289.

XX (AMTY-) AMERICAN TYPE CULTURE COLLECTION.

XX Roblin RO;

XX WPI; 1997-020833/02.

XX Two-stage PCR system using sets of mixed and single sequence primers

XX - useful for sensitive detection of mycobacteria and

XX mycobacteria-like organism contamination of nucleic acid samples

XX Claim 18; Page 30; 42pp; English.

XX The present sequence is the M34 primer involved in the second stage of  
CC PCR in the novel method for amplifying a target segment of nucleic acid  
CC in a sample nucleic acid mixture. It is part of the second stage primer  
CC mixture that is made up of 3 different primers:- F2, R2, and M34 in  
CC relative molar ratios of 0.25; 0.125; 1. Using both first and second  
CC stage primers in the nested PCR method provides an enhanced system for  
CC specific, sensitive and rapid detection of the presence and  
CC identification of Mycoplasma species and Mycoplasma-like organism (MLO)  
CC contaminants contained in a sample of nucleic acid. The method allows  
CC detection of less than 200 colony forming units (cfu)/ml of Mycoplasma  
CC species M.fermentans, M.hyorhinis, M.arginini, M.pirum, M.hominis and  
CC M.salivarium and 350 cfu/ml for M. orale. This compares to detection  
CC levels of 1000 cfu/ml for known Mycoplasma detection systems. Also,  
CC unlike prior art Mycoplasma detection systems, the new method and  
CC primers can detect the MLO contaminant Acholeplasma laidlawii at  
CC levels as low as 20 cfu/ml.

XX Sequence 22 BP; 1 A; 8 C; 4 G; 9 T; 0 other;

Query Match 76.0%; Score 11.4; DB 18; Length 22;  
Best Local Similarity 92.3%; Pred. No. 2e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggggtcacagtgg 15  
| | | | | | | | | | |  
Db 13 GGGCACACAGTGG 1

Search completed: October 2, 2001, 16:18:47  
Job time: 15491 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:53 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20

Sequence: 1 catgatgcttaaaagcttac 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_NA:\*
- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
  - 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
  - 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
  - 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-20
2	15	75.0	15	3	US-09-377-310-40
3	13.8	69.0	29	1	US-08-244-492A-7
4	13.8	69.0	29	1	US-08-709-915-9
5	13.4	67.0	44	2	US-08-818-604-5
6	13.2	66.0	33	1	US-08-285-936-14
7	13.2	66.0	33	1	US-08-487-860-14
8	13.2	66.0	33	2	US-08-762-308-5
9	13.2	66.0	33	5	PCT-US95-04221-5
10	12.6	63.0	36	3	US-08-961-083-418
11	12.4	62.0	20	4	US-09-488-671-75
12	12.2	61.0	25	1	US-08-348-891A-10
13	12.2	61.0	25	1	US-08-505-817-10
14	12.2	61.0	27	3	US-08-985-162-1042
15	12.2	61.0	27	3	US-08-964-268-13
16	12.2	61.0	29	2	US-08-871-266B-4
17	12.2	61.0	29	2	US-08-819-458A-6
18	12.2	61.0	29	2	US-09-018-864A-4
19	12.2	61.0	29	3	US-08-871-267B-6
20	12.2	61.0	29	4	US-08-821-994-24
21	12.2	61.0	30	1	US-08-583-318-2
22	12.2	61.0	33	3	US-08-868-594-5
23	12.2	61.0	33	3	US-08-961-083-330
24	12.2	61.0	33	4	US-09-305-408-3
25	12	60.0	31	3	US-08-961-083-272
26	12	60.0	34	3	US-08-961-083-316
27	12	60.0	42	6	5256642-28

28	12	60.0	42	6	5472939-28	Patent No. 5472939
29	12	60.0	44	2	US-08-327-451E-29	Sequence 29, Appl
30	12	60.0	44	2	US-08-458-109-29	Sequence 29, Appl
31	11.8	59.0	21	2	US-08-487-867-31	Sequence 31, Appl
32	11.8	59.0	21	5	PCT-US96-09358-31	Sequence 31, Appl
33	11.8	59.0	27	3	US-08-985-162-1497	Sequence 1497, Ap
34	11.8	59.0	30	1	US-07-832-905B-84	Sequence 84, Appl
35	11.8	59.0	30	2	US-08-700-757-84	Sequence 84, Appl
36	11.8	59.0	34	2	US-08-521-871A-7	Sequence 7, Appli
37	11.8	59.0	37	2	US-08-202-044-28	Sequence 28, Appl
38	11.8	59.0	37	4	US-08-751-344B-27	Sequence 27, Appl
39	11.8	59.0	45	2	US-08-244-434-8	Sequence 8, Appli
40	11.6	58.0	21	4	US-09-581-493-6	Sequence 6, Appli
41	11.6	58.0	23	2	US-09-100-398-1	Sequence 1, Appli
42	11.6	58.0	25	2	US-08-828-010-8	Sequence 8, Appli
43	11.6	58.0	26	2	US-08-373-284A-3	Sequence 3, Appli
44	11.6	58.0	26	2	US-08-514-542C-9	Sequence 9, Appli
45	11.6	58.0	27	3	US-08-985-162-1512	Sequence 1512, Ap

ALIGNMENTS

RESULT 1  
US-09-377-310-20  
; Sequence 20, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-20

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20  
|||||

Db 1 catgatgcttaaaagcttac 20  
|||||

RESULT 2  
US-09-377-310-40  
; Sequence 40, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence



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RESULT 5
US-08-818-604-5
; Sequence 5, Application US/08818604C
; Patent No. 5958713
; GENERAL INFORMATION:
; APPLICANT: Thastrup, Ole
; APPLICANT: Tullin, Soren
; APPLICANT: Poulsen, Lars
; APPLICANT: Bjorn, Sara
; TITLE OF INVENTION: A Method Of Detecting Biologically
; FILE REFERENCE: 4301.204-US
; CURRENT APPLICATION NUMBER: US/08/818,604C
; CURRENT FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 0110/95
; EARLIER FILING DATE: 1995-01-31
; EARLIER APPLICATION NUMBER: 0982/95
; EARLIER FILING DATE: 1995-09-07
; EARLIER APPLICATION NUMBER: PCT/DK96/00052
; EARLIER FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-08-818-604-5

Query Match 67.0%; Score 13.4; DB 2; Length 44;
Best Local Similarity 93.3%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 atgcttaaaagctta 19
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Db 5 atcttaaaagctta 19

RESULT 6
US-08-285-936-14/c
; Sequence 14, Application US/08285936
; Patent No. 5728821
; GENERAL INFORMATION:
; APPLICANT: Yelton, Dale
; APPLICANT: Glaser, Scott
; APPLICANT: Huse, William
; APPLICANT: Rosok, Mae J.
; TITLE OF INVENTION: No. 5728821el Mutant BR96 Antibodies and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,936
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.16US01
; TELECOMMUNICATION INFORMATION:
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,936
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.16US01
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-285-936-14

Query Match 66.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagcttac 20
| ||| |||||
Db 28 TTATGCCTAAAGCTTTC 11

RESULT 7
US-08-487-860-14/c
; Sequence 14, Application US/08487860
; Patent No. 5792456
; GENERAL INFORMATION:
; APPLICANT: Yelton, Dale
; APPLICANT: Glaser, Scott
; APPLICANT: Huse, William
; APPLICANT: Rosok, Mae J.
; TITLE OF INVENTION: No. 5792456el Mutant BR96 Antibodies and
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,860
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.16US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-487-860-14

Query Match 66.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagcttac 20
| ||| |||||
Db 28 TTATGCCTAAAGCTTTC 11
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RESULT 8  
US-08-762-308-5/c  
; Sequence 5, Application US/08762308  
; Patent No. 5925548  
; GENERAL INFORMATION:  
; APPLICANT: Beutler, Bruce A.  
; APPLICANT: Bazzoni, Flavia M.  
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY  
; TITLE OF INVENTION: SIGNAL  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/762.308  
; FILING DATE: 09-DEC-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/224,593  
; FILING DATE: 05-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UFSO-335--1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 418-3000  
; TELEFAX: 474-7577  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-762-308-5

Query Match 66.0%; Score 13.2; DB 2; Length 33;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 atgatgcttaaaagctta 19  
| ||||| |||||  
Db 23 AGGATGCTTGGAGCTTA 6

RESULT 9  
PCT-US95-04221-5/c  
; Sequence 5, Application PC/TUS9504221  
; GENERAL INFORMATION:  
; APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS  
; APPLICANT: NAME:  
; APPLICANT: SYSTEM  
; APPLICANT: STREET: 201 West 7th Street  
; APPLICANT: CITY: Austin  
; APPLICANT: STATE: Texas  
; APPLICANT: COUNTRY: United States of America  
; APPLICANT: POSTAL CODE: 78701  
; APPLICANT: TELEPHONE NO: (512) 499-4462  
; APPLICANT: TELEFAX: (512) 499-4523  
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT  
; TITLE OF INVENTION: CONTINUOUSLY SIGNAL

; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04221  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US SN 08/224,593  
; FILING DATE: 05 APRIL 1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KITCHELL, BARBARA S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UFTD335P--  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
PCT-US95-04221-5

Query Match 66.0%; Score 13.2; DB 5; Length 33;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 atgatgcttaaaagctta 19  
| ||||| |||||  
Db 23 AGGATGCTTGGAGCTTA 6

RESULT 10  
US-08-961-083-418/c  
; Sequence 418, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961.083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 418:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-083-418

Query Match 63.0%; Score 12.6; DB 3; Length 36;
Best Local Similarity 78.9%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 atgatgcttaaaagcttac 20
|| ||| | | |||||
Db 21 ATTATGTTGATAAGCTTAC 3

RESULT 11
; US-09-488-671-75
; Sequence 75, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
; FILE REFERENCE: RTS-0123
; CURRENT APPLICATION NUMBER: US/09/488,671A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-488-671-75

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 9.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gatgcttaaaagct 17
||||| |||||
Db 1 gatgctgaaaagct 14

RESULT 12
; US-08-348-891A-10/c
; Sequence 10, Application US/08348891A
; Patent No. 5654136
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,817
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; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,891A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,400
; FILING DATE: 10-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-293625
; FILING DATE: 14-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: KP-7501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-348-891A-10

Query Match 61.0%; Score 12.2; DB 1; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagct 17
||||| |||
Db 25 CATGATGCTTGAGAGGT 9

RESULT 13
; US-08-905-817-10/c
; Sequence 10, Application US/08905817
; Patent No. 5824777
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,817
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; FILING DATE: 04-AUG-1997;  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 08/348,891  
; FILING DATE: 25-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,400  
; FILING DATE: 10-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-293625  
; FILING DATE: 14-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: KP-7501A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-521-2297  
; TELEFAX: 703-685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-905-817-10

Query Match 61.0%; Score 12.2; DB 1; Length 25;  
Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catgatgtcttaaaagct 17  
||||||| | | |  
Db 25 CATGATGCTTGAGAGT 9

RESULT 14  
US-08-985-162-1042  
; Sequence 1042, Application US/08985162  
; Patent No. 6057156  
; GENERAL INFORMATION:  
; APPLICANT: Akhtar, Saghir  
; APPLICANT: Fell, Patricia  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT  
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
; NUMBER OF SEQUENCES: 1877  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,162  
; FILING DATE: 04 December 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/036,476  
; FILING DATE: 31 January 1997  
; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 230/107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1042:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: The letter "N" stands for the stem  
; OTHER INFORMATION: II region of a HH ribozyme.  
US-08-985-162-1042

Query Match 61.0%; Score 12.2; DB 3; Length 27;  
Best Local Similarity 55.6%; Pred. No. 1.2e+03;  
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 tgatgcttaaaagcttac 20  
: || : | | | | | : |  
Db 10 UGAUGANGAAAAAGCUUC 27

RESULT 15  
US-08-964-268-13/c  
; Sequence 13, Application US/08964268  
; Patent No. 6114503  
; GENERAL INFORMATION:  
; APPLICANT: WEI, YING-PEI  
; APPLICANT: RUBEN, STEVEN M  
; APPLICANT: SANCAR, AZIZ  
; APPLICANT: HSU, SHIAO-WEN D  
; APPLICANT: KAZANTSEV, ALEKSEY G  
; TITLE OF INVENTION: HUMAN BLUE-LIGHT PHOTORECEPTOR HCXY2  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,268  
; FILING DATE: HEREWITH  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/030,189  
; FILING DATE: 04-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0750001/EKS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-964-268-13

Query Match 61.0%; Score 12.2; DB 3; Length 27;  
Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atgatgcttaaaagctt 18  
| | | | | | | | | | | | | | | | | | | | |  
Db 20 AGGATGCCTGAAAGCTT 4

Search completed: October 2, 2001, 16:03:53  
Job time: 14597 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:45 ; Search time 876.95 seconds  
(without alignments)  
14.320 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20

Sequence: 1 catgatgcttaaaagcttac 20

Scoring table:

IDENTITY\_NUC

Gap 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID58/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
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21: /SID58/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID58/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65552 Human focal adhesi
2	16.4	82.0	26	22	AAF81601 Bacterial 16S rRNA
3	15	75.0	15	22	AAC65572 Human focal adhesi
4	14.2	71.0	29	21	AAZ38455 Helicobacter pylori
5	13.8	69.0	27	20	AAZ221085 Staphylococcus aur
6	13.8	69.0	29	14	AAQ42521 Anti-sense strand
7	13.6	68.0	48	19	AAV43258 Primer used to amp
8	13.4	67.0	44	17	AAZ39690 cAMP receptor prot
9	13.2	66.0	20	17	AAZ27603 Anti-metastatic fu
10	13.2	66.0	20	17	AAZ12926 Human serum albumi
11	13.2	66.0	22	21	AAZ50168 3'PCR primer for i

c 12	13.2	66.0	33	16	AAT00817 5' 75 kD TNF recep
c 13	13.2	66.0	33	20	AAZ25353 Mouse A1 T cell re
c 14	13.2	66.0	40	21	AAA56045 Plasmid pLAC11-rec
c 15	13	65.0	32	21	AAA60654 Human HNRCP PCR pr
c 16	12.8	64.0	27	18	AAZ67579 Human flt1 VEGF re
c 17	12.8	64.0	32	18	AAZ49498 FokI cleavage doma
c 18	12.8	64.0	34	19	AAV33065 Human tissue facto
c 19	12.8	64.0	34	20	AAZ78677 Ribozyme vector ol
c 20	12.8	64.0	36	20	AAZ78691 Plasmid insert pGE
c 21	12.8	64.0	42	20	AAZ78693 Ribozyme vector ol
c 22	12.8	64.0	42	20	AAZ78676 Ribozyme vector ol
c 23	12.8	64.0	42	20	AAZ78675 Ribozyme vector ol
c 24	12.6	63.0	27	18	AAZ70589 Human KDR VEGF rec
c 25	12.6	63.0	27	18	AAZ67769 Human flt1 VEGF re
c 26	12.6	63.0	30	21	AAA11245 Primer p4 for anne
c 27	12.6	63.0	31	21	AAZ00870 3' primer to gener
c 28	12.6	63.0	31	21	AAZ00874 AAV2/4 bottom prim
c 29	12.6	63.0	35	18	AAT62943 Primer for DNA enc
c 30	12.6	63.0	36	19	AAV39935 Streptococcus pneu
c 31	12.6	63.0	36	19	AAV01477 Prion protein forw
c 32	12.6	63.0	36	19	AAV01479 Prion protein forw
c 33	12.6	63.0	36	22	AAZ59530 Mouse prion protei
c 34	12.6	63.0	36	22	AAZ59532 Human prion protei
c 35	12.6	63.0	50	20	AAZ52031 Synthetic plasmid
c 36	12.4	62.0	20	22	AAZ62919 Human PEPCK-cytoso
c 37	12.2	61.0	19	18	AAT69751 Corn starch branch
c 38	12.2	61.0	19	21	AAA82839 cdk4 ribozyme bind
c 39	12.2	61.0	19	21	AAA82840 cdk4 ribozyme bind
c 40	12.2	61.0	19	21	AAA82841 cdk4 ribozyme bind
c 41	12.2	61.0	25	21	AAZ34652 Human growth facto
c 42	12.2	61.0	27	18	AAZ70719 Human KDR VEGF rec
c 43	12.2	61.0	27	18	AAZ68287 Human flt1 VEGF re
c 44	12.2	61.0	27	19	AAZ98262 Human EGF-R hammer
c 45	12.2	61.0	27	19	AAZ43570 Human blue-light p

#### ALIGNMENTS

#### RESULT 1

ID AAC65552 standard; DNA; 20 BP.  
XX  
AC AAC65552;  
XX  
XX  
DF 12-FEB-2001 (first entry)  
XX  
DE Human focal adhesion kinase antisense sequence #18.  
XX  
XX Human; focal adhesion kinase; FAK; signal transduction; cancer;  
KW embryonic development disorder; angiogenic disorder; wound healing;  
KW antisense; phosphothioate; ss.  
XX  
OS Homo sapiens.  
XX  
XX US6133031-A.  
XX  
PD 17-OCT-2000.  
XX  
XX  
PF 19-AUG-1999; 99US-0377310.  
XX  
PR 19-AUG-1999; 99US-0377310.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Gaarde WA;  
XX  
DR WPI; 2001-006141/01.  
XX  
XX  
PT New antisense compounds for inhibiting focal adhesion kinase  
PT expression, especially useful for inhibiting retinal  
PT neovascularization, or for diagnosing and treating e.g. colon cancer -  
XX

PS Claim 3; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
 CC is involved in integrin-mediated signal transduction, and is implicated  
 CC in cancer, particularly colon, breast and oral tumours, embryonic  
 CC development disorders, angiogenic disorders and wound healing. The  
 CC antisense sequences, including the one shown here, can be used in the  
 CC treatment of all of these.

XX Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.73;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20  
 |||||

Db 1 catgatgcttaaaagcttac 20

#### RESULT 2

AAF81601/c  
 ID AAF81601 standard; DNA; 26 BP.

AC AAF81601;

XX 05-JUN-2001 (first entry)

DE Bacterial 16S rRNA coding sequence PCR primer RVR-3.

XX Probe; PCR primer; 16S rRNA; bacterial detection; Microbispora;  
 KW Microtetraspora; Nonomuria; Planobispora; ss.

XX Microbispora.

OS Microtetraspora.

OS Planobispora.

XX WO200123608-A2.

XX 05-APR-2001.

PF 25-SEP-2000; 2000WO-BP09459.

XX 27-SEP-1999; 99US-0156171.

XX (MERI ) MERCK SHARP & DOHME ESPANA SAE.

PI Genilloud O, Mellado RP, Parro V, Rodriguez V;

DR WPI; 2001-281685/29.

XX Novel nucleic acid probe hybridizing to nucleic acid encoding portion  
 PT of 16S rRNA of bacteria of genera Microbispora, Microtetraspora,  
 PT Nonomuria and Planobispora, useful for detecting these bacteria in  
 PT sample -

PS Disclosure; Page 9; 20pp; English.

XX The present invention provides several probes and PCR primers which can  
 CC be used in the detection of bacteria belonging to the genera of  
 CC Microbispora, Microtetraspora, Nonomuria and Planobispora. The sequences  
 CC hybridise to the 16S rRNA coding sequence of the organism. The present  
 CC sequence is a PCR primer of the invention.

XX Sequence 26 BP; 7 A; 8 C; 5 G; 6 T; 0 other;

Query Match 82.0%; Score 16.4; DB 22; Length 26;  
 Best Local Similarity 94.4%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagctt 18  
 |||||

Db 18 CATGTTGCTTAAAGCTT 1

#### RESULT 3

AAC65572  
 ID AAC65572 standard; DNA; 15 BP.

XX AAC65572;

XX 12-FEB-2001 (first entry)

DE Human focal adhesion kinase antisense sequence #38.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;  
 KW embryonic development disorder; angiogenic disorder; wound healing;  
 KW antisense; phosphorothioate; ss.

XX Homo sapiens.

XX US6133031-A.

XX 17-OCT-2000.

XX 19-AUG-1999; 99US-0377310.

PR 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

PA Monia BP, Gaarde WA;

PI WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase  
 PT expression, especially useful for inhibiting retinal  
 PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX Example 2; Column 25; 30pp; English.

CC The present invention describes a number of phosphorothioate antisense  
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
 CC is involved in integrin-mediated signal transduction, and is implicated  
 CC in cancer, particularly colon, breast and oral tumours, embryonic  
 CC development disorders, angiogenic disorders and wound healing. The  
 CC antisense sequences, including the one shown here, can be used in the  
 CC treatment of all of these.

XX Sequence 15 BP; 5 A; 2 C; 3 G; 5 T; 0 other;

Query Match 75.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagct 17  
 |||||

Db 1 tgatgcttaaaagct 15

#### RESULT 4

AAZ38455/c  
 ID AAZ38455 standard; DNA; 29 BP.

XX AAZ38455;

XX 22-FEB-2000 (first entry)

DE Helicobacter pylori neutrophil activating protein (NAP) PCR primer #2.

XX Neutrophil activating protein; NAP; stomach; ulcer; cancer; neutrophil;  
 KW activation; adhesion; inflammatory response; inflammation;

KW cloning artefact; salting out; ammonium sulphate;  
 KW metal chelate chromatography; therapy; diagnosis; therapeutic agent;  
 KW vaccine; immunoassay; immunodiagnosis; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 OS Helicobacter pylori.  
 XX  
 PN WO9953310-A1.  
 XX  
 PD 21-OCT-1999.  
 XX  
 XX 07-APR-1999; 99WO-IB00695.  
 PF  
 XX 08-APR-1998; 98GB-0007721.  
 PR  
 XX (CHIR-) CHIRON SPA.  
 PA  
 PI Grandi G;  
 XX  
 DR WPI; 2000-052659/04.  
 XX  
 XX Enriching presence of Helicobacter pylori neutrophil activating  
 PT protein, useful in diagnostic and therapeutic products and processes  
 PT  
 XX Disclosure; Page 8; 26pp; English.  
 PS  
 XX This sequence represents NAP PCR primer #2, used with primer #1  
 CC (AAZ38454) to amplify DNA (AAZ38453) encoding the neutrophil activating  
 CC protein (NAP) from Helicobacter pylori strain CCUG. The PCR product  
 CC was then cloned into the Escherichia coli and Bacillus subtilis  
 CC shuttle vector pSM214G for recombinant production. In humans  
 CC infected with H. pylori, NAP promotes activation and adhesion  
 CC of neutrophils to endothelial cells, an inflammatory response.  
 CC Since H. pylori is responsible for stomach inflammation, it is possible  
 CC that NAP elicits the inflammatory response, probably at an early stage  
 CC of gastric ulcer disease, when neutrophils accumulate in the superficial  
 CC gastric mucosa. The invention relates to a novel process for enriching  
 CC the presence of Helicobacter pylori NAP in a mixture of proteins. This  
 CC comprises the steps of salting out other proteins (NAP being soluble at  
 CC 80% ammonium sulphate saturation) and metal chelate chromatography  
 CC (preferably with immobilised nickel cations). The NAP purified or  
 CC enriched in this way is free from amino acid sequences or alterations  
 CC introduced during cloning (e.g., polyhistidine tags, thioredoxin fusions  
 CC or GST fusions). NAP produced via this process may be useful for the  
 CC production of therapeutic agents, such as vaccines. It may also be  
 CC useful in an immunoassay to ascertain antibody levels in a body sample,  
 CC and in immunodiagnosis kits.  
 XX  
 SQ Sequence 29 BP; 8 A; 8 C; 4 G; 9 T; 0 other;  
 XX  
 Query Match 71.0%; Score 14.2; DB 21; Length 29;  
 Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 catgatgcttaaaagctta 19  
 ||| |||||  
 DB 23 CATTTGGCTTAAAGCTTA 5  
 RESULT 5  
 AAZ21085/c  
 ID AAZ21085 standard; DNA; 27 BP.  
 XX  
 AC AAZ21085;  
 XX  
 DT 17-NOV-1999 (first entry)  
 DE  
 DE Staphylococcus aureus trxB PCR primer #2.  
 XX  
 XX Staphylococcus; trxB; thioredoxin reductase; antimicrobial;  
 KW PCR primer; ss.  
 XX

OS Synthetic.  
 OS Staphylococcus aureus.  
 XX  
 PN WO9945123-A1.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 02-MAR-1999; 99WO-US04512.  
 XX  
 XX 02-MAR-1998; 98US-0076525.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Aharonowitz Y, Borovok I, Cohen G, Uziel O, Katz L;  
 PI  
 XX WPI; 1999-551044/46.  
 DR  
 XX A new thioredoxin reductase from Staphylococcus aureus  
 PT  
 XX Example 3; Page 32; 59pp; English.  
 PS  
 XX The present invention describes Staphylococcus thioredoxin reductase  
 CC (trxB). The present sequence represent a PCR primer for S. aureus trxB.  
 CC trxB inhibitors can be used as antimicrobials to treat a Staphylococcus,  
 CC particularly S. aureus, infection. trxB inhibitors are antimicrobials to  
 CC which, unlike most of those in the prior art, Staphylococcus has not yet  
 CC developed a resistance.  
 CC  
 XX Sequence 27 BP; 7 A; 6 C; 4 G; 10 T; 0 other;  
 SQ  
 Query Match 69.0%; Score 13.8; DB 20; Length 27;  
 Best Local Similarity 88.2%; Pred. No. 7.2e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 atgatgcttaaaagctt 18  
 ||| |||||  
 DB 20 ATCAAGCTTAAAGCTT 4  
 RESULT 6  
 AAQ42521/c  
 ID AAQ42521 standard; DNA; 29 BP.  
 XX  
 AC AAQ42521;  
 XX  
 DT 27-SEP-1993 (first entry)  
 DE  
 DE Anti-sense strand of the coding sequence of human 7B2.  
 XX  
 XX 7B2; chaperone function; deaggregation; PCR; ss.  
 KW  
 XX Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS complement (9..29)  
 FT /\*tag= a  
 XX  
 XX WO9311248-A.  
 PN  
 XX 10-JUN-1993.  
 PD  
 XX 27-NOV-1992; 92WO-EP02740.  
 PF  
 XX 29-NOV-1991; 91NL-0002009.  
 PR  
 XX (UYKA-) UNIV STICHTING KATHOLIEKE.  
 PA (CIBA ) CIBA GEIGY AG.  
 XX  
 XX Martens GJM, Chaudhuri B, Stephan C;  
 PI  
 XX WPI; 1993-197066/24.  
 DR  
 XX

PT Efficient expression and de-aggregation of protein - by treating  
PT co-expressing protein, e.g. hormone, growth or coagulation factor  
PT or neuro-peptide with 7B2  
XX  
PS Example; Page 36; 41pp; English.  
XX  
CC The source of the DNA is partly human genomic DNA whilst the  
CC immediate experimental source is synthetic. AAQ42515 and AAQ42521 are  
CC used in the construction of a truncated 7B2 gene encoding an  
CC amino terminal 7B2 signal peptide and the first 170 AAs of the  
CC human protein. They are used as primers in a PCR using complete  
CC human cDNA.  
XX  
SQ Sequence 29 BP; 11 A; 6 C; 3 G; 9 T; 0 other;

Query Match 69.0%; Score 13.8; DB 14; Length 29;  
Best Local Similarity 88.2%; Pred. No. 7.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagctta 19  
|| ||| ||||| |||||  
Db 18 TGTGCTATAAAGCTTA 2

RESULT 7  
AAV43258  
ID AAV43258 standard; DNA; 48 BP.  
XX  
AC AAV43258;  
XX  
DT 27-OCT-1998 (first entry)  
XX  
DE Primer used to amplify plasmid pK5DT.  
XX  
KW Non-covalent complex; antibody; immunoglobulin; immunogen; vaccine;  
KW cytotoxic; expression agent; treatment; cancer; expression; transgene;  
KW primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9834956-A1.  
XX  
PD 13-AUG-1998.  
XX  
PF 06-FEB-1998; 98WO-FR00227.  
XX  
PR 07-FEB-1997; 97FR-0001420.  
XX  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
XX  
PI Drevet P, Leonetti M, Menez A;  
XX  
DR WPI; 1998-447169/38.  
XX  
PT New non-covalent complex of targeting antibody and immunoglobulin  
PT binding component - linked to active agent, e.g. antigen, drug or  
PT nucleic acid, used for treatment of cancer  
PS  
PS Example 6; Page 20; 42pp; French.  
XX  
CC AAV43257-58 represent primers used to amplify plasmid pK5DT. The  
CC specification describes a non-covalent complex that comprises at  
CC least one antibody, or its fragments, able to bind a cell-surface  
CC molecule and a component that binds (to only 1 type of site) an  
CC immunoglobulin (Ig) or fragment, and is associated with an active  
CC substance. The complexes are used as immunogens, vaccines or as  
CC cytotoxic or expression agents, e.g. for treatment of cancer or  
CC for expressing transgenes.  
XX  
SQ Sequence 48 BP; 14 A; 9 C; 10 G; 15 T; 0 other;

Query Match 68.0%; Score 13.6; DB 19; Length 48;  
Best Local Similarity 80.0%; Pred. No. 9.3e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20  
|| ||| ||||| |||||  
Db 8 caggatcctataaagctcc 27

RESULT 8  
AAT39690  
ID AAT39690 standard; DNA; 44 BP.  
XX  
AC AAT39690;  
XX  
DT 04-APR-1997 (first entry)  
XX  
DE CAMP receptor protein DNA, PCR primer.  
XX  
KW Green fluorescent protein; detection; active substance; affecting;  
KW intracellular process; fluorescence; probe; screen; identification;  
KW luminescent; real time; study; second messenger; enzyme; primer;  
KW protein kinase; PCR; polymerase chain reaction; CAMP; receptor;  
KW protein; ss.  
XX  
OS Synthetic.  
XX  
PN WO9623898-A1.  
XX  
PD 08-AUG-1996.  
XX  
PF 31-JAN-1996; 96WO-DK00052.  
XX  
PR 07-SEP-1995; 95DK-0000982.  
PR 31-JAN-1995; 95DK-0000110.  
XX  
PA (NOVO ) NOVO-NORDISK AS.  
XX  
PI Bjorn SP, Poulsen LK, Thastrup O, Tullin S;  
XX  
DR WPI; 1996-371444/37.  
XX  
PT New construct encoding modified green fluorescent protein - contg.  
PT e.g. enzyme recognition site, useful for detecting biologically  
PT active substances affecting intracellular processes  
XX  
PS Example 3; Page 20; 48pp; English.  
XX  
CC A claimed fusion construct containing sequences encoding the  
CC Aequorea victoria green fluorescent protein (GFP) and a portion of  
CC the CAMP receptor protein, i.e. a sequence PCR amplified using the  
CC PCR primer pair AAT39689/90, can be used for the detection of a  
CC biologically active substance affecting intracellular processes.  
CC A cell containing the construct is cultured under conditions  
CC permitting GFP expression, and its fluorescence measured. The cell  
CC is then incubated with the substance, and its fluorescence  
CC measured, where any change indicates that the substance is  
CC biologically active. The construct can also be used to generate  
CC probes for use in basic research, and screening programmes to  
CC identify new biologically active substances. The use of  
CC luminescent probes allows real time studies of 2nd messengers and  
CC specific enzymes, e.g. protein kinases, in single living cells,  
CC making possible the study of the precise timing and spatial  
CC characteristics of these factors. Due to the strong fluorescence  
CC of GFP, the luminescence of cells expressing the probes, which  
CC are easily introduced into cells, can be easily detected and  
CC analysed.  
XX  
SQ Sequence 44 BP; 12 A; 8 C; 11 G; 13 T; 0 other;

Query Match 67.0%; Score 13.4; DB 17; Length 44;  
Best Local Similarity 93.3%; Pred. No. 1.2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 atgcttaaaagctta 19  
||| ||||| |||||  
Db 5 attcttaaaagctta 19

RESULT 9  
AAT27603/c  
ID AAT27603 standard; DNA; 20 BP.  
XX  
AC AAT27603;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
XX Anti-metastatic fusion protein-encoding vector construction primer.

XX Cancer; metastasis; fusion protein; non-disruptional; inhibitor;  
KW arbitrary insertion; human serum albumin; HSA; PCR;  
KW polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
PN JF08053500-A.

XX  
PD 27-FEB-1996.  
XX  
XX  
PF 11-AUG-1994; 94JP-0209368.  
XX  
PR 11-AUG-1994; 94JP-0209368.  
XX  
PA (ASAG ) ASAHI GLASS CO LTD.

XX WPI; 1996-175732/18.

XX Fusion protein comprising human serum albumin contg. peptide  
PT inserted at arbitrary position - useful for, e.g. inhibiting cancer  
PT metastasis

XX Example 5; Page 21; 24pp; Japanese.

XX AAT27602-T27615 are PCR primers used for the construction of vectors  
CC carrying human serum albumin (HSA) fusion proteins (FPs). The HSA  
CC FPs contain a peptide capable of inhibiting metastasis of cancerous  
CC cells. The primers are used to introduce restriction sites into the  
CC HSA gene for efficient expression and recovery of the FP. Introduction  
CC of the anti-metastatic peptide does not destroy the stereo structure  
CC of HSA. Previously such fusion proteins could only be produced by a  
CC combination of a chemical synthetic method and a binding method.  
CC Using recombinant DNA technology for FP prodn. provides a steady  
CC supply of the fusion protein on an industrial scale.

XX Sequence 20 BP; 6 A; 3 C; 2 G; 9 T; 0 other;

Query Match 66.0%; Score 13.2; DB 17; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atgctgcttaaaagctta 19  
||| | | |||||  
Db 20 ATGAAGATCAAAAGCTTA 3

RESULT 10  
AAT12926/c  
ID AAT12926 standard; DNA; 20 BP.

XX  
AC AAT12926;

XX 23-AUG-1996 (first entry)

DE Human serum albumin gene PCR primer.

XX HSA: modify; mutagenesis; genetic engineering; fusion gene;  
KW restriction endonuclease; recognition site; amplification;  
KW polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
XX JP08051982-A.  
XX  
PD 27-FEB-1996.  
XX  
XX 11-AUG-1994; 94JP-0209369.  
PF  
XX 11-AUG-1994; 94JP-0209369.  
PR  
XX (ASAG ) ASAHI GLASS CO LTD.  
PA  
XX WPI; 1996-174566/18.  
DR  
XX Human serum albumin gene modified by introduction of restriction  
PT site - useful for production of fusion proteins by inserting active  
PT peptide coding sequence into new restriction site  
XX  
XX Example 2 and 3; Page 17; 19pp; Japanese.

XX Restriction enzyme recognition sites are introduced into the human  
CC serum albumin gene at one or more positions to facilitate  
CC preparation of fusion genes. The restriction sites are pref.  
CC introduced at the N-terminus, the C-terminus, between the first and  
CC second domains and/or between the second and third domains of HSA.  
CC The modified HSA gene can then readily be fused to a sequence coding  
CC for a physiologically active peptide, e.g. a cancer metastasis  
CC inhibitor. The present sequence is that of a PCR primer which was  
CC used in the construction of coding sequences AAT12919 and AAT12920  
CC which had restriction sites introduced into the gene at positions  
CC corresp. to the region between domains 1 and 2 or between domains 2  
CC and 3, respectively.

XX Sequence 20 BP; 6 A; 3 C; 2 G; 9 T; 0 other;

Query Match 66.0%; Score 13.2; DB 17; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atgctgcttaaaagctta 19  
||| | | |||||  
Db 20 ATGAAGATCAAAAGCTTA 3

RESULT 11  
AAZ50168/c  
ID AAZ50168 standard; DNA; 22 BP.

XX  
AC AAZ50168;

XX 04-MAY-2000 (first entry)

XX 3'PCR primer for isolation and characterisation of P. pastoris FLD1 gene.  
XX Methyiotrophic yeast; formaldehyde dehydrogenase 1; FLD1; marker;  
KW formaldehyde resistance; PCR primer; ss.  
KW  
XX Pichia pastoris.

OS

XX WO200001829-A2.

XX 13-JAN-2000.

XX 02-JUL-1999; 99WO-US15016.

XX 03-JUL-1998; 98US-0091699.

```

PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
PI Cregg JW;
XX
XX WPI; 2000-182118/16.
XX
XX New formaldehyde dehydrogenase gene for methylotrophic yeast, useful as
PT selection marker, also its promoter for regulated expression of
PT heterologous polypeptides
XX
XX Example 2; Page 46; 101pp; English.
XX
XX The present sequence is a 3' PCR primer used in RT-PCR to amplify
CC intron corresponding region from total P. pastoris mRNA, for isolation
CC and characterisation of formaldehyde dehydrogenase 1 (FLD1) gene. FLD
CC protects cells from toxic effects of formaldehyde and imparts
CC formaldehyde resistance. It is therefore useful as a selectable marker
CC in methylotrophic yeast. Expression cassettes comprising FLD regulatory
CC sequences (promoter and terminator) can be used to control the
CC expression of heterologous proteins in transformed methylotrophic
CC yeast cells. Formaldehyde resistant host cells can be selected by
CC transforming them with a vector comprising FLD gene operably linked to
CC a heterologous promoter and growing them in the presence of formaldehyde.
XX
XX Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 other;
SQ
Query Match 66.0%; Score 13.2; DB 21; Length 22;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 tgatgcttaaaagcttac 20
Db | | | | | | | | | |
21 TGATGCTTACACGCTTTC 4
RESULT 12
AAT00817/c
ID AAT00817 standard; DNA; 33 BP.
AC AAT00817;
XX
XX 13-MAY-1996 (first entry)
DT
DE 5' 75 kD TNF receptor primer.
XX
XX Tumour necrosis factor; TNF; erythropoietin receptor; EpoR; cytokine;
KW tumour therapy; polymerase chain reaction; PCR; primer; amplify; ss.
XX
XX Synthetic.
OS
XX WO9526985-A1.
PN
XX 12-OCT-1995.
PD
XX 05-APR-1995; 95WO-US04221.
PF
XX 05-APR-1994; 94US-0224593.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Bazzoni FM, Beutler BA;
PI
XX WPI; 1995-358585/46.
XX
XX New constructs for stimulating signalling in cells - comprising a
PT cytokine receptor cytoplasmic domain linked to a multimerising
PT extracellular domain
XX
XX Example 5; Page 16; 42pp; English.
PS
XX AAT00817 and AAT00818 are amplification primers for the stem,
XX transmembrane and cytoplasmic domains of the 75 kD tumour necrosis factor
CC

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CC (TNF) receptor. AAT00815 and AAT00816 amplify the 55 kD TNF receptor.
CC The amplified sequence is used in a chimeric protein with the
CC erythropoietin receptor (EpoR) sequence amplified by AAT00813 and
CC AAT00814. A vector that expresses a chimeric receptor, such as the one
CC created using the amplified sequence, can be used to induce a cytotoxic
CC effect in a cell. The chimeric receptor can be used for the treatment of
CC tumours, and to provide a model for studying the formation of tumours.
CC By altering the extracellular and transmembrane domains of the chimeric
CC protein, the target sequence is changed. The formation of multimeric
CC receptor complexes on the extracellular surface, when the chimeric
CC protein is used, is sufficient for transmitting a positive signal to the
CC cytoplasmic domain of the receptor. This occurs even in the absence of
CC the cognate ligand, or in the presence of a ligand that has entirely
CC different activities. The advantage with using the chimeric protein is
CC that the response of the cytokine (in this case TNF) can be induced
CC without side effects.
XX
XX Sequence 33 BP; 8 A; 10 C; 6 G; 9 T; 0 other;
SQ
Query Match 66.0%; Score 13.2; DB 16; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 atgatgcttaaaagctta 19
Db | | | | | | | | | |
23 AGGATGCTTGAAGCTTA 6
RESULT 13
AAX25353
ID AAX25353 standard; DNA; 33 BP.
XX
XX AC AAX25353;
XX
XX 19-JUL-1999 (first entry)
DT
DE Mouse A1 T cell receptor beta chain PCR primer.
XX
XX T cell receptor beta chain; mouse; transgenic animal;
KW animal model; immunological tolerance; graft rejection;
KW tissue grafting; neonatal intolerance; transplantation antigen;
KW H-Y antigen; PCR; primer; ss.
XX
XX Synthetic.
OS
XX Mus musculus.
XX
XX WO9916867-A1.
PN
XX PD 08-APR-1999.
XX
XX 30-SEP-1998; 98WO-GB02965.
PF
XX 01-OCT-1997; 97GB-0020888.
PR
XX (ISIS-) ISIS INNOVATION LTD.
PA
XX Cobbold SP, Waldmann H, Zelenika D;
PI
XX WPI; 1999-255090/21.
XX
XX Transgenic non-human mammal having only CD4 positive T cells
PT specific for at least one transplantation antigen, useful for
PT studying immunological tolerance
XX
XX Example 1; Page 9; 41pp; English.
PS
XX This oligonucleotide was used as a primer for the PCR amplification
CC of a cDNA clone (see AAX25358) coding for the T cell receptor (TCR)
CC beta chain (see AAY05728) from the A1 CD4+ T cell clone isolated
CC from CBA/Ca mice. The A1 clone recognises the minor
CC histocompatibility antigen H-Y present in male, but absent in
CC female, mice. The amplified product was used in the construction
CC

```

CC of Al(M) transgenic mice. The invention relates to a transgenic  
 CC animal model comprising TCR alpha and beta chains. It provides a  
 CC genetically modified non-human mammal having a population of CD4  
 CC positive T cells specific for one or a limited number of selected  
 CC antigens, including at least transplantation antigen capable of  
 CC rejecting a tissue transplant containing the transplantation  
 CC antigen and, if applicable, the other selected antigens. The  
 CC animal has TCR genes which encode a TCR specific for the  
 CC transplantation antigen. The animal is useful for studying  
 CC immunological tolerance, especially the mechanisms of tolerance to,  
 CC and the rejection of, tissue grafts, and in pregnancy. The animals  
 CC are also useful for testing agents for biological activity in  
 CC promoting or reducing immunological tolerance.  
 XX  
 SQ Sequence 33 BP; 10 A; 5 C; 9 G; 9 T; 0 other;  
 Query Match 66.0%; Score 13.2; DB 20; Length 33;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 catgatgcttaaaagctt 18  
 Db 8 caggatgcataaaagttt 25  
 RESULT 14  
 ID AAA56045/c  
 XX AAA56045 standard; DNA; 40 BP.  
 AC AAA56045;  
 XX  
 DT 05-SEP-2000 (first entry)  
 XX  
 DE Plasmid pLAC11-recA construction PCR primer SEQ ID NO:17.  
 XX  
 KW Escherichia coli; E. coli; randomised peptide library; identification;  
 KW stabilised bioactive peptide; synthesis; intracellular selection;  
 KW screening; lac operon; protease resistant; peptidase resistant;  
 KW Rop protein; glutathione sulphotransferase; thioredoxin; infection;  
 KW maltose binding protein; glutathione reductase; antimicrobial;  
 KW antibacterial; PCR primer; ss.  
 XX  
 OS Escherichia coli.  
 OS Synthetic.  
 XX  
 PN W0200022112-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 XX 12-OCT-1999; 99WO-US23731.  
 XX  
 XX 13-OCT-1998; 98US-0104013.  
 PR 14-DEC-1998; 98US-0112150.  
 XX  
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA (ALTM/) ALTMAN E.  
 XX  
 PI Altman E.  
 XX  
 DR WPI; 2000-317972/27.  
 XX  
 XX Identifying recombinantly an antimicrobial bioactive peptide used as a  
 PT therapeutic agent involves transforming a host cell with expression  
 PT vector with tightly regulable control region and measuring its  
 PT inhibition.  
 XX  
 PS Example 1; Page 36; 135pp; English.  
 XX  
 CC The present invention describes a method for identifying a bioactive  
 CC peptide (BP) involving transforming a cell with an expression vector  
 CC comprising a tightly regulable control region operably linked to a  
 CC nucleic acid sequence encoding a peptide (P), growing the transformed

CC cell under conditions that repress expression of (P) and then inducing  
 CC its expression which, if is inhibitory to host cell growth, is  
 CC indicative of BP expression. An antimicrobial peptide from the present  
 CC invention, which is stabilised, is used for treating a patient having a  
 CC condition treatable with a peptide drug. The stabilised peptides are  
 CC also used for inhibiting the growth of a microbe. The new antibacterial  
 CC peptides are useful to treat various pathogenic bacteria such as  
 CC Staphylococci, Streptococci and Enterococci which are the primary causes  
 CC of nosocomial infections. Novel inhibitor peptides identified by the  
 CC method can be medical treatments and therapies directed against  
 CC microbial infection. Also, these novel inhibitor peptides can be used,  
 CC in turn, to identify additional novel antibacterial peptides using a  
 CC synthetic approach, and can also be used to elucidate potential new drug  
 CC targets. The inhibitor peptide target which is inactivated is identified  
 CC using reverse genetics by isolating mutants that are no longer inhibited  
 CC by the peptide. These mutants are then mapped in order to precisely  
 CC determine the protein target that is inhibited. AAA56033 to AAA56106 and  
 CC AAY90964 to AAY90999 are sequences used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 40 BP; 12 A; 6 C; 5 G; 17 T; 0 other;  
 Query Match 66.0%; Score 13.2; DB 21; Length 40;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 atgatgcttaaaagctta 19  
 Db 23 AAGATTTTAAAGCTTA 6  
 RESULT 15  
 ID AAA60654/c  
 XX AAA60654 standard; DNA; 32 BP.  
 AC AAA60654;  
 XX  
 DT 24-OCT-2000 (first entry)  
 XX  
 XX Human HNRCR PCR primer SEQ ID NO:26.  
 DE  
 XX Human; HNRCR; nuclear receptor coreceptor; PCR primer; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX CN1250094-A.  
 PN  
 XX 12-APR-2000.  
 PD  
 XX 06-OCT-1998; 98CN-0120919.  
 PF  
 XX 06-OCT-1998; 98CN-0120919.  
 PR  
 XX (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.  
 PA  
 XX Yu L, Tu Q, Zhao Y;  
 PI  
 XX WPI; 2000-400830/35.  
 DR  
 XX Preparation of new human kernon acceptor co-repressor coding series and  
 PT the polypeptide -  
 PT  
 XX Example 3; Page 11; 58pp; Chinese.  
 PS  
 XX The present invention describes a human homologue of nuclear receptor  
 CC coreceptor (HNRCR). The present sequence represents a PCR primer for  
 CC human HNRCR, which is used in an example from the present invention.  
 CC  
 XX Sequence 32 BP; 11 A; 7 C; 8 G; 6 T; 0 other;  
 SQ  
 Query Match 65.0%; Score 13; DB 21; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 tgcttaaaagctt 18  
|||||  
Db 17 TGCTTAAAGCTT 5

Search completed: October 2, 2001, 16:18:46  
Job time: 15490 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:52 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-18

Perfect score: 20

Sequence: 1 ttccaaccagatggtcattc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-18
2	15	75.0	15	3	US-09-377-310-38
3	14.2	71.0	20	3	US-09-357-071-39
4	12.8	64.0	25	3	US-08-762-428A-10
5	12.8	64.0	29	1	US-08-306-871-32
6	12.8	64.0	29	1	US-08-569-959-32
7	12.6	63.0	35	1	US-08-469-005A-7
8	12.4	62.0	26	3	US-08-938-835A-41
9	12.4	62.0	30	1	US-08-463-975-4
10	12.4	62.0	30	1	US-08-783-266-4
11	12.4	62.0	30	2	US-09-023-327-4
12	12.2	61.0	20	1	US-08-531-556-4
13	12.2	61.0	20	1	US-08-472-416-4
14	12.2	61.0	23	4	US-09-101-886B-30
15	12.2	61.0	28	2	US-08-859-998-1026
16	12.2	61.0	33	2	US-08-479-275D-38
17	12.2	61.0	33	2	US-08-488-271B-38
18	12.2	61.0	34	2	US-08-612-840A-9
19	12.2	61.0	20	3	US-09-377-310-43
20	12.2	61.0	25	4	US-09-586-935-17
21	12.2	61.0	25	4	US-08-685-376-11
22	11.8	59.0	25	2	US-08-117-952-499
23	11.8	59.0	28	4	US-08-957-621-3
24	11.8	59.0	35	2	US-08-818-604-24
25	11.8	59.0	38	2	US-08-857-946-106
26	11.8	59.0	38	3	US-08-970-740-106
27	11.8	59.0	38	4	US-09-262-773-45

c 28	11.8	59.0	39	4	US-09-342-749-18	Sequence 18, Appl
c 29	11.6	58.0	23	1	US-08-133-711-24	Sequence 24, Appl
c 30	11.6	58.0	32	1	US-08-276-852-15	Sequence 15, Appl
31	11.6	58.0	32	1	US-08-133-011-22	Sequence 22, Appl
32	11.6	58.0	32	1	US-08-322-730A-22	Sequence 22, Appl
33	11.6	58.0	32	1	US-08-162-102C-3	Sequence 3, Appl
34	11.6	58.0	32	1	US-08-387-874-22	Sequence 22, Appl
35	11.6	58.0	32	1	US-08-899-575-15	Sequence 15, Appl
36	11.6	58.0	32	1	US-08-899-575-15	Sequence 15, Appl
37	11.6	58.0	32	2	US-08-383-619-22	Sequence 22, Appl
38	11.6	58.0	32	4	US-08-907-739-22	Sequence 22, Appl
39	11.6	58.0	32	5	PCT-US93-08364-22	Sequence 3, Appl
40	11.6	58.0	32	5	PCT-US95-00067-3	Sequence 3, Appl
41	11.6	58.0	32	5	PCT-US95-08743-15	Sequence 15, Appl
42	11.6	58.0	33	2	US-08-896-410-30	Sequence 30, Appl
c 43	11.6	58.0	38	1	US-08-276-852-20	Sequence 20, Appl
c 44	11.6	58.0	38	1	US-08-133-011-27	Sequence 27, Appl

## ALIGNMENTS

RESULT 1

US-09-377-310-18

; Sequence 18, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; APPLICANT: Gaarde, William A.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; TITLE OF INVENTION: Expression

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377.310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antisense sequence

US-09-377-310-18

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.087;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ttccaaccagatggtcattc 20

|||||

Db 1 ttccaaccagatggtcattc 20

RESULT 2

US-09-377-310-38

; Sequence 38, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; APPLICANT: Gaarde, William A.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; TITLE OF INVENTION: Expression

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377.310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 38

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: antisense sequence  
US-09-377-310-38

Query Match 75.0%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcaaccagatggtca 17  
|||||

Db 1 tcaaccagatggtca 15

RESULT 3  
US-09-357-071-39  
Sequence 39, Application US/09357071  
Patent No. 6043091  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
FILE REFERENCE: RTS-0074  
CURRENT APPLICATION NUMBER: US/09/357,071  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 39  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-357-071-39

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 83;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ttccaaccagatggtcatt 19  
|||

Db 1 ttccaaccagatggtcatt 19

RESULT 4  
US-08-762-428A-10  
Sequence 10, Application US/08762428A  
Patent No. 6120993  
GENERAL INFORMATION:  
APPLICANT: Ye, Guo-jie  
APPLICANT: Breslow, Esther M.  
APPLICANT: Meister, Alton  
TITLE OF INVENTION: 5-OXOPROLINASE  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/762,428A  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: TIMIAN, SUSAN J.  
REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/1330  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-762-428A-10

Query Match 64.0%; Score 12.8; DB 3; Length 25;  
Best Local Similarity 87.5%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtca 17  
|||||

Db 8 ttcaaccatattggca 23

RESULT 5  
US-08-306-871-32  
Sequence 32, Application US/08306871  
Patent No. 5712118  
GENERAL INFORMATION:  
APPLICANT: Timothy F. Murphy  
TITLE OF INVENTION: Vaccine For Brnhamella catarrhalis  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1  
SOFTWARE: Wordperfect for Windows 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,871  
FILING DATE: 20-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/129,719  
FILING DATE: September 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 11520.0053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Brnhamella catarrhalis  
STRAIN: 25240  
US-08-306-871-32

Query Match 64.0%; Score 12.8; DB 1; Length 29;  
Best Local Similarity 87.5%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtca 17

Db 10 TTCATCCAGATGATCA 25  
||||| ||||| |||

## RESULT 6

US-08-569-959-32  
; Sequence 32, Application US/08569959  
; Patent No. 5725862  
; GENERAL INFORMATION:  
; APPLICANT: Timothy F. Murphy  
; TITLE OF INVENTION: Vaccine For Branhamella catarrhalis  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1  
; SOFTWARE: Wordperfect for Windows 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569,959  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/129,719  
; FILING DATE: September 29, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 11520.0053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single-stranded  
; TOPOLOGY: linear  
; ORGANISM: Branhamella catarrhalis  
; STRAIN: 25240  
US-08-569-959-32

Query Match 64.0%; Score 12.8; DB 1; Length 29;  
Best Local Similarity 87.5%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtcca 17  
||||| ||||| |||

Db 10 TTCATCCAGATGATCA 25

## RESULT 7

US-08-469-005A-7/c  
; Sequence 7, Application US/08469005A  
; Patent No. 5665874  
; GENERAL INFORMATION:  
; APPLICANT: KUHAJDA, FRANCIS P.  
; APPLICANT: PASTERNAK, GARY A.  
; TITLE OF INVENTION: CANCER RELATED ANTIGEN  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAKER & BOTTS, L.L.P.  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC

; COUNTRY: USA  
; ZIP: 20004-2400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,005A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/188,426  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 08/096,908  
; FILING DATE: 26-JUL-1993  
; APPLICATION NUMBER: 07/917,716  
; FILING DATE: 24-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Posorske, Laurence H  
; REGISTRATION NUMBER: 34,698  
; REFERENCE/DOCKET NUMBER: 062482-0113  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-639-7700  
; TELEFAX: 202-639-7890  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
US-08-469-005A-7

Query Match 63.0%; Score 12.6; DB 1; Length 35;  
Best Local Similarity 78.9%; Pred. No. 5.9e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtcattc 20  
||||| ||||| ||||| |||

Db 35 TTCAGAAGATGGCCATGC 17

## RESULT 8

US-08-938-835A-41/c  
; Sequence 41, Application US/08938835A  
; Patent No. 6060245  
; GENERAL INFORMATION:  
; APPLICANT: SORGE, Joseph A.  
; APPLICANT: MULLINAX, Rebecca L.  
; TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING  
; TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner, L.L.P.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,835A  
FILING DATE: 26-SEPT-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/775,993  
FILING DATE: 03-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/779,335  
FILING DATE: 06-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Barker, M. Paul  
REGISTRATION NUMBER: 32,013  
REFERENCE/DOCKET NUMBER: 04121.0044-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-938-835A-41

Query Match 62.0%; Score 12.4; DB 3; Length 26;  
Best Local Similarity 92.9%; Pred. No. 7.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 caacagatgttca 17  
|||||

Db 18 CAACAGATGTGCA 5

RESULT 9  
US-08-463-975-4  
Sequence 4, Application US/08463975  
Patent No. 5618717  
GENERAL INFORMATION:  
APPLICANT: WEI, ET AL.  
TITLE OF INVENTION: HABH  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,975  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/12058  
FILING DATE: 21 OCT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-331  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1744  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 BASE PAIRS

TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Oligonucleotide  
US-08-463-975-4

Query Match 62.0%; Score 12.4; DB 1; Length 30;  
Best Local Similarity 92.9%; Pred. No. 7.4e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttccaacagatgg 14  
|||||

Db 9 TTTCATCCAGATGG 22

RESULT 10  
US-08-783-266-4  
Sequence 4, Application US/08783266  
Patent No. 5747312  
GENERAL INFORMATION:  
APPLICANT: WEI, ET AL.  
TITLE OF INVENTION: HABH  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,266  
FILING DATE: 15-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/463,975  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: PCT/US94/12058  
FILING DATE: 21 OCT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-331  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Oligonucleotide  
US-08-783-266-4

Query Match 62.0%; Score 12.4; DB 1; Length 30;  
Best Local Similarity 92.9%; Pred. No. 7.4e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttccaacagatgg 14  
|||||

Db 9 TTTCATCCAGATGG 22

RESULT 11

```
US-09-023-327-4
; Sequence 4, Application US/09023327
; Patent No. 5929225
; GENERAL INFORMATION:
; APPLICANT: WEI, ET AL.
; TITLE OF INVENTION: HABH
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,327
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,975
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: PCT/US94/12058
; FILING DATE: 21 OCT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: Oligonucleotide
US-09-023-327-4

Query Match 62.0%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ttcaaccagatgg 14
Db 9 TTTCATCCAGATGG 22

RESULT 12
US-08-531-556-4
; Sequence 4, Application US/08531556
; Patent No. 5776682
; GENERAL INFORMATION:
; APPLICANT: Agoulnik, Alexander I
; APPLICANT: Kent First, Marijo
; APPLICANT: Muallem, Ariege
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; ZIP: 53717-1914

US-09-023-327-4

Query Match 61.0%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtcat 18
Db 1 TCCATCCAGCTGGTCAT 17

RESULT 13
US-08-472-416-4
; Sequence 4, Application US/08472416
; Patent No. 5783390
; GENERAL INFORMATION:
; APPLICANT: Agoulnik, A.
; APPLICANT: Kent, Marijo G.
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472.416
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

US-08-531-556-4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,556
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.034CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: DNA (genomic)
US-08-531-556-4
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; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-472-416-4

Query Match 61.0%; Score 12.2; DB 1; Length 20;  
Best Local Similarity 82.4%; Pred. No. 8.9e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ttcaaccagatggtcat 18  
| | | | | | | | | |  
Db 1 TCCATCCAGCTGTCAT 17

## RESULT 14

US-09-101-886B-30  
; Sequence 30, Application US/09101886B  
; Patent No. 6197507  
; GENERAL INFORMATION:  
; APPLICANT: BERG, THOMAS  
; APPLICANT: TOLLERSRUD, OLE K  
; APPLICANT: NILSEN, OIVIND  
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BARBARA G. ERNST  
; STREET: 555 13TH STREET, NW SUITE 701E  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/101,886B  
; FILING DATE: 29-JANUARY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB97/00109  
; FILING DATE: 12-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1181-240  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES

US-09-101-886B-30

Query Match 61.0%; Score 12.2; DB 4; Length 23;  
Best Local Similarity 82.4%; Pred. No. 9e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 tcaaccagatggtcatt 19  
| | | | | | | | | |  
Db 6 TCATCCAGTTGGTCAAT 22

## RESULT 15

US-08-859-998-1026  
; Sequence 1026, Application US/08859998  
; Patent No. 5994076  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Jokhadze, George  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,998  
; FILING DATE: 21-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Field, Bret E.  
; REGISTRATION NUMBER: 37,620  
; REFERENCE/DOCKET NUMBER: 09096/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-322-5070  
; TELEFAX: 415-854-0875  
; INFORMATION FOR SEQ ID NO: 1026:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-1026

Query Match 61.0%; Score 12.2; DB 2; Length 28;  
Best Local Similarity 82.4%; Pred. No. 9.3e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ttcaaccagatggtcat 18  
| | | | | | | | | |  
Db 3 TTCTACCAAGGTGTCAT 19

Search completed: October 2, 2001, 16:03:53  
Job time: 14597 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:45 ; Search time 876.95 Seconds  
(without alignments)  
14.320 Million cell updates/sec

Title: US-09-757-100B-18

Perfect score: 20

Sequence: 1 tttcaaccagatggtcattc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0601:\*  
1: /SIDS8/gcgdata/geneseq/geneseq/NA1980.DAT:\*  
2: /SIDS8/gcgdata/geneseq/geneseq/NA1981.DAT:\*  
3: /SIDS8/gcgdata/geneseq/geneseq/NA1982.DAT:\*  
4: /SIDS8/gcgdata/geneseq/geneseq/NA1983.DAT:\*  
5: /SIDS8/gcgdata/geneseq/geneseq/NA1984.DAT:\*  
6: /SIDS8/gcgdata/geneseq/geneseq/NA1985.DAT:\*  
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11: /SIDS8/gcgdata/geneseq/geneseq/NA1990.DAT:\*  
12: /SIDS8/gcgdata/geneseq/geneseq/NA1991.DAT:\*  
13: /SIDS8/gcgdata/geneseq/geneseq/NA1992.DAT:\*  
14: /SIDS8/gcgdata/geneseq/geneseq/NA1993.DAT:\*  
15: /SIDS8/gcgdata/geneseq/geneseq/NA1994.DAT:\*  
16: /SIDS8/gcgdata/geneseq/geneseq/NA1995.DAT:\*  
17: /SIDS8/gcgdata/geneseq/geneseq/NA1996.DAT:\*  
18: /SIDS8/gcgdata/geneseq/geneseq/NA1997.DAT:\*  
19: /SIDS8/gcgdata/geneseq/geneseq/NA1998.DAT:\*  
20: /SIDS8/gcgdata/geneseq/geneseq/NA1999.DAT:\*  
21: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:\*  
22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65550 Human focal adhesi
2	15	75.0	15	22	AAC65570 Human focal adhesi
3	14.4	72.0	38	20	AA86411 PCR primer PDZK5.5
4	14.2	71.0	20	21	AAAI4039 Human liver glyco
5	13.8	69.0	41	19	AAV51245 Maize polymorphic
6	13.8	69.0	41	19	AAV51246 Maize polymorphic
7	13.8	69.0	41	19	AAV47956 Maize polymorphic
8	13.8	69.0	41	19	AAV47957 Maize polymorphic
9	13.4	67.0	41	19	AAV51243 Maize polymorphic
10	13.4	67.0	41	19	AAV51244 Maize polymorphic
11	13.4	67.0	41	19	AAV47954 Maize polymorphic

c 12	13.4	67.0	41	19	AAV47955	Maize polymorphic
c 13	13.2	66.0	33	21	AA255314	Neisseria species
c 14	13.2	66.0	50	20	AA252031	Synthetic plasmid
c 15	12.8	64.0	25	19	AAV28114	Rat 5-oxoprolinase
c 16	12.8	64.0	25	21	AA253025	Human beta-1,3-gal
c 17	12.8	64.0	25	21	AA253029	Human beta-1,3-gal
c 18	12.8	64.0	29	16	AA091896	B.cattarrhalis CD e
c 19	12.8	64.0	29	21	AA04221	Polymorphic fragme
c 20	12.8	64.0	38	15	AA073036	Tyrosine-kinase sy
c 21	12.8	64.0	38	15	AA073037	Tyrosine-kinase sy
c 22	12.6	63.0	31	21	AA229977	PCR primer used in
c 23	12.6	63.0	35	18	AA288208	Probe used in prep
c 24	12.6	63.0	35	20	AA215118	Probe used to isol
c 25	12.6	63.0	35	20	AA203260	Probe used to isol
c 26	12.6	63.0	41	18	AA278192	Micro gene random
c 27	12.6	63.0	47	21	AA287025	RBP-7 biallelic ma
c 28	12.4	62.0	23	22	AA290273	Primer #17 used in
c 29	12.4	62.0	24	10	AA292881	ER-specific probe.
c 30	12.4	62.0	26	19	AA240115	PCR primer used to
c 31	12.4	62.0	30	17	AA272968	Primer for amplif
c 32	12.4	62.0	30	18	AA268318	Human homologue of
c 33	12.4	62.0	30	20	AA288777	Human AlkB homolog
c 34	12.4	62.0	46	21	AA266377	Chitinase specific
c 35	12.4	62.0	46	21	AA272653	Chitinase degenera
c 36	12.2	61.0	20	18	AA272839	SPT6 homologue for
c 37	12.2	61.0	20	18	AA268289	Locl-specific prim
c 38	12.2	61.0	27	20	AA272185	Human NBC PCR prim
c 39	12.2	61.0	29	21	AA240437	Polymorphic fragme
c 40	12.2	61.0	30	20	AA272184	Human NBC PCR prim
c 41	12.2	61.0	30	21	AA288895	Human wolframin in
c 42	12.2	61.0	42	20	AA286407	PCR primer PDZK5.4
c 43	12	60.0	14	21	AA26147	Oestrogen receptor
c 44	12	60.0	20	21	AA266803	Dog genomic marker
c 45	12	60.0	20	22	AA265575	Human focal adhesi

#### ALIGNMENTS

RESULT 1  
AAC65550  
ID. AAC65550 standard; DNA; 20 BP.  
XX  
AC AAC65550;  
XX  
DT 12-FEB-2001 (first entry)  
XX  
DE Human focal adhesion kinase antisense sequence #16.  
XX  
KW Human; focal adhesion kinase; FAK; signal transduction; cancer;  
KW embryonic development disorder; angiogenic disorder; wound healing;  
KW antisense; phosphothioate; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6133031-A.  
XX  
PD 17-OCT-2000.  
XX  
PF 19-AUG-1999; 99US-0377310.  
XX  
PR 19-AUG-1999; 99US-0377310.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Gaarde WA;  
XX  
DR WPI; 2001-006141/01.  
XX  
PT New antisense compounds for inhibiting focal adhesion kinase  
PT expression, especially useful for inhibiting retinal  
XX neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Claim 3; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
CC is involved in integrin-mediated signal transduction, and is implicated  
CC in cancer, particularly colon, breast and oral tumours, embryonic  
CC development disorders, angiogenic disorders and wound healing. The  
CC antisense sequences, including the one shown here, can be used in the  
CC treatment of all of these.

XX Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0; Indels 0; Gaps 0;

Qy 1 tttcaaccagatggtcattc 20

Db 1 tttcaaccagatggtcattc 20

RESULT 2

AAC65570

ID AAC65570 standard; DNA; 15 BP.

AC AAC65570;

XX 12-FEB-2001 (first entry)

DE Human focal adhesion kinase antisense sequence #36.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX Homo sapiens.

XX US6133031-A.

XX 17-OCT-2000.

XX 19-AUG-1999; 99US-0377310.

XX 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX Example 2; Column 25; 30pp; English.

PS The present invention describes a number of phosphorothioate antisense

CC sequences to the human focal adhesion kinase (FAK) protein. This protein

CC is involved in integrin-mediated signal transduction, and is implicated

CC in cancer, particularly colon, breast and oral tumours, embryonic

CC development disorders, angiogenic disorders and wound healing. The

CC antisense sequences, including the one shown here, can be used in the

CC treatment of all of these.

XX Sequence 15 BP; 5 A; 4 C; 3 G; 3 T; 0 other;

Query Match 75.0%; Score 15; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcaaccagatggtca 17

Db 1 tcaaccagatggtca 15

RESULT 3

AA86411/c

ID AA86411 standard; DNA; 38 BP.

XX AC AA86411;

XX 29-SEP-1999 (first entry)

DE PCR primer PDZK5.5Q used to amplify DNA encoding MMSC1 protein.

KW Human; MMSC1 protein; MMAC1 interacting protein; tumour suppression;

KW MMAC1 pathway; immunogen; cancer; cell neoplastic growth; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9936566-A1.

XX 22-JUL-1999.

XX 19-JAN-1999; 99WO-US00995.

XX 20-JAN-1998; 98US-0071861.

XX (MYRI-) MYRIAD GENETICS INC.

XX Bartel PL, Tavtigian SV;

XX WPI; 1999-458472/38.

XX MMSC1, an MMAC1 (tumour suppressor) interacting protein and related

XX polynucleotides

XX Example 5; Page 50; 107pp; English.

XX PCR primers AAX86368-X86423 were used to amplify DNA encoding a human

CC MMSC1 protein. The PCR templates were derived from tumour cell lines,

CC and the amplicons were tested for mutations. The MMSC1 protein is a

CC MMAC1 interacting protein which is involved in tumour suppression

CC activity in the MMAC1 pathway. MMSC1, antigenic fragments or fusion

CC proteins of these are used as immunogens for antibody production. Primers

CC derived from MMSC1 genomic clones can be used for identification of MMSC1

CC genes and for synthesis by amplification of MMSC1 DNA or RNA. Detecting

CC an alteration in MMSC1 can be used to diagnose cancer. A germline

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

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CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

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CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

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CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

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CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.

AAAL14039  
 ID AAA14039 standard; DNA; 20 BP.  
 AC AAA14039;  
 XX  
 DT 18-JUL-2000 (first entry)  
 XX  
 DE Human liver glycogen phosphorylase antisense oligo, SEQ ID NO:39.  
 XX  
 KW Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;  
 KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;  
 KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;  
 KW expression inhibition; hypoglycaemic; type II diabetes;  
 KW non insulin-dependent; antisense; phosphorothioate; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 XX  
 PN US6043091-A.  
 XX  
 PD 28-MAR-2000.  
 XX  
 PF 19-JUL-1999; 99US-0357071.  
 XX  
 PR 19-JUL-1999; 99US-0357071.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Cowsert LM;  
 XX  
 DR WPI; 2000-270346/23.  
 XX  
 PT Antisense compounds particularly oligonucleotides useful for  
 PT prophylaxis, diagnosis and treatment of diseases associated with  
 PT expression of liver glycogen phosphorylase  
 XX  
 PS Claim 3; Column 40; 33pp; English.  
 XX  
 CC Sequences AAA14008-A14047 represent phosphorothioate antisense  
 CC oligonucleotides targeted to the human liver glycogen phosphorylase  
 CC gene (PYGL gene), which inhibit its expression. The antisense  
 CC oligonucleotides were designed to target different regions of human  
 CC liver glycogen phosphorylase RNA, and were analysed for their effect  
 CC on liver glycogen phosphorylase levels by quantitative real-time PCR.  
 CC Liver glycogen phosphorylase is one of three glycogen phosphorylase  
 CC isozymes, which differ in their tissue-specific distribution,  
 CC immunological properties and electrophoretic mobilities and are  
 CC encoded by three different genes. Liver glycogen phosphorylase is  
 CC glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate  
 CC alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active  
 CC form) catalyses the degradation of stored glycogen in the liver to  
 CC glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds.  
 CC It therefore plays a critical role in carbohydrate metabolism and blood  
 CC glucose homeostasis. Inhibition of liver glycogen phosphorylase and  
 CC therefore glycogenolysis may provide a means of reducing blood glucose  
 CC levels in diabetic patients, particularly those with type II (non  
 CC insulin-dependent) diabetes. The antisense oligonucleotides  
 CC of the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with liver glycogen phosphorylase expression, or  
 CC those which may benefit from inhibition of liver glycogen phosphorylase  
 CC expression, such as type II diabetes.  
 XX  
 SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 other;  
 XX  
 Query Match 71.0%; Score 14.2; DB 21; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ttccaccagatggtcatt 19  
 || ||||| |||||  
 Db 1 ttccaccatagggtcatt 19  
 || ||||| |||||  
 RESULT 5  
 ID AAV51245 standard; DNA; 41 BP.  
 XX  
 AC AAV51245;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Maize polymorphic marker S02G2/GS-2 DNA.  
 XX  
 KW Polymorphic marker; allele-specific; primer; probe; amplification;  
 KW hybridisation; plant; hybrid certification; genetic contribution;  
 KW progeny; back-cross; hybrid; ancestry; maize; ss.  
 XX  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 FT variation 21  
 FT /\*tag= a  
 FT /replace= "c"  
 FT /note= "polymorphism"  
 XX  
 PN WO9824796-A1.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 01-DEC-1997; 97WO-US21782.  
 XX  
 PR 07-MAR-1997; 97US-0813507.  
 PR 02-DEC-1996; 96US-0032069.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;  
 XX  
 DR WPI; 1998-333252/29.  
 XX  
 CC Brassica species allele-specific oligonucleotide probes and primers  
 CC - useful for plant breeding  
 XX  
 PS Claim 1; Page 49; 65pp; English.  
 XX  
 CC This DNA sequence is a region of a Zea mays genome which contains a  
 CC polymorphic marker. This sequence can be used in the construction of  
 CC allele-specific primers and probes for amplification or hybridisation,  
 CC e.g. to determine common or disparate ancestry between 2 or more plants,  
 CC to monitor the genetic contribution of an ancestral plant, to trace the  
 CC progeny of proprietary plants, in certification of a hybrid plant or to  
 CC identify the progeny of a back-crossed plant with an ancestral plant.  
 XX  
 SQ Sequence 41 BP; 8 A; 8 C; 13 G; 12 T; 0 other;  
 XX  
 Query Match 69.0%; Score 13.8; DB 19; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 4.2e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 caaccagatggtcatt 20  
 || ||||| |||||  
 Db 22 CCACGAGATGTCATC 6  
 || ||||| |||||  
 RESULT 6  
 ID AAV51246 standard; DNA; 41 BP.  
 XX  
 AC AAV51246;  
 XX

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XX 11-JAN-1999 (first entry)
DT
XX
XX Maize polymorphic marker S02G2/G5-2B DNA.
DE
XX
XX Polymorphic marker; allele-specific; primer; probe; amplification;
KW hybridisation; plant; hybrid certification; genetic contribution;
KW progeny; back-cross; hybrid; ancestry; maize; ss.
XX
OS Zea mays.
XX
XX Key Location/Qualifiers
FH variation 21
FT /*tag= a
FT /replace= "c"
FT /note= "polymorphism"
XX
PN WO9824796-A1.
XX
XX 11-JUN-1998.
PD
XX
XX 01-DEC-1997; 97WO-US21782.
XX
XX 07-MAR-1997; 97US-0813507.
PR
XX 02-DEC-1996; 96US-0032069.
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;
PI
XX WPI; 1998-333252/29.
XX
XX Brassica species allele-specific oligonucleotide probes and primers
PT - useful for plant breeding
PT
XX Claim 1; Page 49; 65pp; English.
PS
XX This DNA sequence is a region of a Zea mays genome which contains a
CC polymorphic marker. This sequence can be used in the construction of
CC allele-specific primers and probes for amplification or hybridisation,
CC e.g. to determine common or disparate ancestry between 2 or more plants,
CC to monitor the genetic contribution of an ancestral plant, to trace the
CC progeny of proprietary plants, in certification of a hybrid plant or to
CC identify the progeny of a back-crossed plant with an ancestral plant.
XX
SQ Sequence 41 BP; 9 A; 9 C; 12 G; 11 T; 0 other;

Query Match 69.0%; Score 13.8; DB 19; Length 41;
Best Local Similarity 88.2%; Pred. NO. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 caaccagatggtcattc 20
Db 22 CCACGAGATGGTCATTC 6

RESULT 7
AAV47956/c
ID AAV47956 standard; DNA; 41 BP.
XX
XX AAV47956;
AC
XX
XX 14-OCT-1998 (first entry)
DT
XX
XX Maize polymorphic site oligonucleotide marker UMC76-G2/G5-2B.
DE
XX
XX Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KW polymorphic site; corn; gramineae species; ss.
XX
XX Synthetic.
OS Zea sp.
XX
XX WO9830717-A2.
PN
XX 16-JUL-1998.
PD

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PN WO9830717-A2.
XX
XX 16-JUL-1998.
PD
XX
XX 02-DEC-1997; 97WO-EP07134.
PF
XX
XX 02-DEC-1996; 96US-0032069.
PR
XX
XX (BIOC-) BIOCEM SA.
PA
XX
XX Murigneux A;
PI
XX WPI; 1998-399160/34.
DR
XX
XX Vegetal sequences including single nucleotide polymorphism - useful,
PT e.g. to determine polymorphisms in plants, determine strain in plant
PT breeding and to correlate polymorphisms with phenotypic traits
XX
XX Claim 2; Page 15; 32pp; English.
PS
XX
XX The present invention describes a nucleic acid segment comprising at
CC least 10 contiguous nucleotides from a vegetal sequence including a
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC complement of the segment. Also described are: (1) an allele-specific
CC oligonucleotides hybridising to segment, or their complements, and (2) a
CC method of analysing nucleic acids from a subject, by determining if a
CC base is occupying any one (or a set) of polymorphic sites in 261
CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with
CC phenotypic traits (e.g. plant growth rate or crop yield), and the
CC segments are useful to determine the presence/absence of specific
CC polymorphisms correlating with the existence/absence of particular
CC traits. The segments are also useful in marker assisted back-cross
CC techniques to select plants with a higher percentage of recurrent parent
CC in a back-cross population. Segments incorporate SNPs which occur more
CC frequently than other polymorphism types and are therefore more likely
CC to be located close to genetic loci of interest; different forms of
CC characterised SNPs are also often easier to detect than other
CC polymorphism types.
XX
SQ Sequence 41 BP; 8 A; 8 C; 12 G; 12 T; 1 other;

Query Match 69.0%; Score 13.8; DB 19; Length 41;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 caaccagatggtcattc 20
Db 22 CSACGAGATGGTCATTC 6

RESULT 8
AAV47957/c
ID AAV47957 standard; DNA; 41 BP.
XX
XX AAV47957;
AC
XX
XX 14-OCT-1998 (first entry)
DT
XX
XX Maize polymorphic site oligonucleotide marker UMC76-G2/G5-2B.
DE
XX
XX Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KW polymorphic site; corn; gramineae species; ss.
XX
XX Synthetic.
OS Zea sp.
XX
XX WO9830717-A2.
PN
XX 16-JUL-1998.
PD

```

XX 02-DEC-1997; 97WO-EP07134.  
 XX 02-DEC-1996; 96US-0032069.  
 XX (BIOC-) BIOCEM SA.  
 XX Murigneux A;  
 XX WPI; 1998-399160/34.  
 XX Vegetal sequences including single nucleotide polymorphism - useful,  
 PT e.g. to determine polymorphisms in plants, determine strain in plant  
 PT breeding and to correlate polymorphisms with phenotypic traits  
 XX Claim 2; Page 15; 32pp; English.  
 CC The present invention describes a nucleic acid segment comprising at  
 CC least 10 contiguous nucleotides from a vegetal sequence including a  
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the  
 CC complement of the segment. Also described are: (1) an allele-specific  
 CC oligonucleotides hybridising to segment, or their complements and (2) a  
 CC method of analysing nucleic acids from a subject, by determining if a  
 CC base is occupying any one (or a set) of polymorphic sites in 261  
 CC sequences derived from six maize lines (see AAV47701 to AAV47961). The  
 CC segments are useful in fingerprint analysis in plants to determine which  
 CC polymorphisms are present, which strain a plant belongs to and to  
 CC distinguish between strains. The polymorphisms may correlate with  
 CC phenotypic traits (e.g. plant growth rate or crop yield), and the  
 CC segments are useful to determine the presence/absence of specific  
 CC polymorphisms correlating with the existence/absence of particular  
 CC traits. The segments are also useful in marker assisted back-cross  
 CC techniques to select plants with a higher percentage of recurrent parent  
 CC in a back-cross population. Segments incorporate SNPs which occur more  
 CC frequently than other polymorphism types and are therefore more likely  
 CC to be located close to genetic loci of interest; different forms of  
 CC characterised SNPs are also often easier to detect than other  
 CC polymorphism types.  
 XX Sequence 41 BP; 9 A; 9 C; 11 G; 11 T; 1 other;  
 SQ

Query Match 69.0%; Score 13.8; DB 19; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 4.2e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 caaccagatggtcattc 20  
 | || |||||  
 Db 22 CSACGATGGTCATTC 6

RESULT 9  
 AAV51243/C  
 ID AAV51243 standard; DNA; 41 BP.  
 AC AAV51243;  
 XX 11-JAN-1999 (first entry)  
 DE Maize polymorphic marker S02G2/G5-1 DNA.  
 XX Polymorphic marker; allele-specific; primer; probe; amplification;  
 KW hybridisation; plant; hybrid certification; genetic contribution;  
 KW progeny; back-cross; hybrid; ancestry; maize; ss.  
 XX Zea mays.  
 OS  
 XX Key Location/Qualifiers  
 FH variation 21  
 FT /\*tag= a  
 FT /replace= "t"  
 FT /note= "polymorphism"

PN WO9824796-A1.  
 XX 11-JUN-1998.  
 XX 01-DEC-1997; 97WO-US21782.  
 XX 07-MAR-1997; 97US-0813507.  
 PR 02-DEC-1996; 96US-0032069.  
 XX (AFFY-) AFFYMETRIX INC.  
 XX Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;  
 XX WPI; 1998-333252/29.  
 XX Brassica species allele-specific oligonucleotide probes and primers  
 PT - useful for plant breeding  
 XX Claim 1; Page 49; 65pp; English.  
 CC This DNA sequence is a region of a Zea mays genome which contains a  
 CC polymorphic marker. This sequence can be used in the construction of  
 CC allele-specific primers and probes for amplification or hybridisation,  
 CC e.g. to determine common or disparate ancestry between 2 or more plants,  
 CC to monitor the genetic contribution of an ancestral plant, to trace the  
 CC progeny of proprietary plants, in certification of a hybrid plant or to  
 CC identify the progeny of a back-crossed plant with an ancestral plant.  
 XX Sequence 41 BP; 8 A; 8 C; 12 G; 13 T; 0 other;  
 SQ

Query Match 67.0%; Score 13.4; DB 19; Length 41;  
 Best Local Similarity 93.3%; Pred. No. 6.8e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 accagatggtcattc 20  
 | |||||  
 Db 40 ACAGATGGTCATTC 26

RESULT 10  
 AAV51244/C  
 ID AAV51244 standard; DNA; 41 BP.  
 XX AAV51244;  
 XX 11-JAN-1999 (first entry)  
 DE Maize polymorphic marker S02G2/G5-1B DNA.  
 XX Polymorphic marker; allele-specific; primer; probe; amplification;  
 KW hybridisation; plant; hybrid certification; genetic contribution;  
 KW progeny; back-cross; hybrid; ancestry; maize; ss.  
 XX Zea mays.  
 OS  
 XX Key Location/Qualifiers  
 FH variation 21  
 FT /\*tag= a  
 FT /replace= "t"  
 FT /note= "polymorphism"

WO9824796-A1.  
 XX 11-JUN-1998.  
 XX 01-DEC-1997; 97WO-US21782.  
 XX 07-MAR-1997; 97US-0813507.  
 PR 02-DEC-1996; 96US-0032069.  
 XX (AFFY-) AFFYMETRIX INC.  
 XX Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;  
 XX WPI; 1998-333252/29.  
 XX Brassica species allele-specific oligonucleotide probes and primers  
 PT - useful for plant breeding  
 XX Claim 1; Page 49; 65pp; English.  
 CC This DNA sequence is a region of a Zea mays genome which contains a  
 CC polymorphic marker. This sequence can be used in the construction of  
 CC allele-specific primers and probes for amplification or hybridisation,  
 CC e.g. to determine common or disparate ancestry between 2 or more plants,  
 CC to monitor the genetic contribution of an ancestral plant, to trace the  
 CC progeny of proprietary plants, in certification of a hybrid plant or to  
 CC identify the progeny of a back-crossed plant with an ancestral plant.  
 XX Sequence 41 BP; 8 A; 8 C; 12 G; 13 T; 0 other;  
 SQ

PI Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;  
 XX WPI; 1998-333252/29.  
 XX Brassica species allele-specific oligonucleotide probes and primers  
 PT - useful for plant breeding  
 XX  
 PS Claim 1; Page 49; 65pp; English.  
 XX This DNA sequence is a region of a Zea mays genome which contains a  
 CC polymorphic marker. This sequence can be used in the construction of  
 CC allele-specific primers and probes for amplification or hybridisation,  
 CC e.g. to determine common or disparate ancestry between 2 or more plants,  
 CC to monitor the genetic contribution of an ancestral plant, to trace the  
 CC progeny of proprietary plants, in certification of a hybrid plant or to  
 CC identify the progeny of a back-crossed plant with an ancestral plant.  
 XX  
 SQ Sequence 41 BP; 8 A; 9 C; 11 G; 13 T; 0 other;  
 Query Match 67.0%; Score 13.4; DB 19; Length 41;  
 Best Local Similarity 93.3%; Pred. No. 6.8e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 accagatggtcattc 20  
 II |||||  
 Db 40 ACGAGATGTCATTC 26  
 RESULT 11  
 AAV47954/c  
 ID AAV47954 standard; DNA; 41 BP.  
 XX AC AAV47954;  
 XX DT 14-OCT-1998 (first entry)  
 XX DE Maize polymorphic site oligonucleotide marker UMC76-G2/G5-1.  
 XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;  
 KW polymorphic site; corn; gramineae species; ss.  
 XX OS Synthetic.  
 OS Zea sp.  
 XX PN WO9830717-A2.  
 XX PD 16-JUL-1998.  
 XX PF 02-DEC-1997; 97WO-EP07134.  
 XX PR 02-DEC-1996; 96US-0032069.  
 XX PA (BIOC-) BIOCEM SA.  
 XX PI Murigneux A;  
 XX WPI; 1998-399160/34.  
 XX Vegetal sequences including single nucleotide polymorphism - useful,  
 PT e.g. to determine polymorphisms in plants, determine strain in plant  
 PT breeding and to correlate polymorphisms with phenotypic traits  
 XX  
 PS Claim 2; Page 15; 32pp; English.  
 XX The present invention describes a nucleic acid segment comprising at  
 CC least 10 contiguous nucleotides from a vegetal sequence including a  
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the  
 CC complement of the segment. Also described are: (1) an allele-specific  
 CC oligonucleotides hybridising to segment, or their complements, and (2) a  
 CC method of analysing nucleic acids from a subject, by determining if a  
 CC base is occupying any one (or a set) of polymorphic sites in 261  
 CC sequences derived from six maize lines (see AAV47701 to AAV47961). The  
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 CC polymorphisms are present, which strain a plant belongs to and to  
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 CC polymorphisms correlating with the existence/absence of specific  
 CC traits. The segments are also useful in marker assisted back-cross  
 CC techniques to select plants with a higher percentage of recurrent parent  
 CC in a back-cross population. Segments incorporate SNPs which occur more  
 CC frequently than other polymorphism types and are therefore more likely  
 CC to be located close to genetic loci of interest; different forms of  
 CC characterised SNPs are also often easier to detect than other  
 CC polymorphism types.  
 XX  
 SQ Sequence 41 BP; 8 A; 8 C; 11 G; 13 T; 1 other;  
 Query Match 67.0%; Score 13.4; DB 19; Length 41;  
 Best Local Similarity 93.3%; Pred. No. 6.8e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 accagatggtcattc 20  
 II |||||  
 Db 40 ACGAGATGTCATTC 26  
 RESULT 12  
 AAV47955/c  
 ID AAV47955 standard; DNA; 41 BP.  
 XX AC AAV47955;  
 XX DT 14-OCT-1998 (first entry)  
 XX DE Maize polymorphic site oligonucleotide marker UMC76-G2/G5-1B.  
 XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;  
 KW polymorphic site; corn; gramineae species; ss.  
 XX OS Synthetic.  
 OS Zea sp.  
 XX PN WO9830717-A2.  
 XX PD 16-JUL-1998.  
 XX PF 02-DEC-1997; 97WO-EP07134.  
 XX PR 02-DEC-1996; 96US-0032069.  
 XX PA (BIOC-) BIOCEM SA.  
 XX PI Murigneux A;  
 XX WPI; 1998-399160/34.  
 XX Vegetal sequences including single nucleotide polymorphism - useful,  
 PT e.g. to determine polymorphisms in plants, determine strain in plant  
 PT breeding and to correlate polymorphisms with phenotypic traits  
 XX  
 PS Claim 2; Page 15; 32pp; English.  
 XX The present invention describes a nucleic acid segment comprising at  
 CC least 10 contiguous nucleotides from a vegetal sequence including a  
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the  
 CC complement of the segment. Also described are: (1) an allele-specific  
 CC oligonucleotides hybridising to segment, or their complements, and (2) a  
 CC method of analysing nucleic acids from a subject, by determining if a  
 CC base is occupying any one (or a set) of polymorphic sites in 261  
 CC sequences derived from six maize lines (see AAV47701 to AAV47961). The  
 CC segments are useful in fingerprint analysis in plants to determine which  
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 CC distinguish between strains. The polymorphisms may correlate with

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 CC segments are useful to determine the presence/absence of specific  
 CC polymorphisms correlating with the existence/absence of particular  
 CC traits. The segments are also useful in marker assisted back-cross  
 CC techniques to select plants with a higher percentage of recurrent parent  
 CC in a back-cross population. Segments incorporate SNPs which occur more  
 CC frequently than other polymorphism types and are therefore more likely  
 CC to be located close to genetic loci of interest; different forms of  
 CC characterised SNPs are also often easier to detect than other  
 CC polymorphism types.

XX  
 SQ Sequence 41 BP; 8 A; 9 C; 10 G; 13 T; 1 other;

Query Match 67.0%; Score 13.4; DB 19; Length 41;

Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 accagatggtcattc 20

|||||||

Db 40 ACGAGATGTCATTC 26

RESULT 13

AAZ55314/c

ID AAZ55314 standard; DNA; 33 BP.

XX

AC AAZ55314;

XX

DT 21-MAR-2000 (first entry)

XX

DE Neisseria species ORF cloning PCR primer #699.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;

KW antibacterial; gene therapy; PCR primer; ss.

XX

OS Synthetic.

OS Neisseria sp.

PN WO9957280-A2.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1999; 99WO-US09346.

XX

PR 01-MAY-1998; 98US-0083758.

PR

PR 31-JUL-1998; 98US-0094869.

PR

PR 02-SEP-1998; 98US-0098994.

PR

PR 02-SEP-1998; 98US-0099062.

PR

PR 09-OCT-1998; 98US-0103749.

PR

PR 09-OCT-1998; 98US-0103794.

PR

PR 09-OCT-1998; 98US-0103796.

PR

PR 25-FEB-1999; 99US-0121528.

XX

XX

PA (CHIR ) CHIRON CORP.

PA

PA (GENO-) INST GENOMIC RES.

XX

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX

DR WPI; 2000-062150/05.

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XX

CC polypeptides, the polynucleotides, antibodies and compositions of  
 CC the invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the  
 CC manufacture of medicaments for treating or preventing infection due to  
 CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the  
 CC presence of Neisseria bacteria, or to raise antibodies. They may also  
 CC be used to screen for agonists or antagonists, which may themselves  
 CC have use as antibacterial agents. The polynucleotides of the invention  
 CC may also be used in gene therapy protocols.

XX  
 SQ Sequence 33 BP; 11 A; 10 C; 4 G; 8 T; 0 other;

Query Match 66.0%; Score 13.2; DB 21; Length 33;

Best Local Similarity 83.3%; Pred. No. 8.3e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tttaaccacagatgcatc 18

|||||

Db 30 TTTGAAATAGATGTCAT 13

RESULT 14

AAZ52031

ID AAZ52031 standard; DNA; 50 BP.

XX

AC AAZ52031;

XX

DT 18-JUN-1999 (first entry)

XX

DE Synthetic plasmid synlux4 construction oligonucleotide F11.

XX

KW DNA plasmid; lux A; lux B; Vibrio fischeri; luciferase; promoter;

KW ttr9 kanamycin/neomycin phosphotransferase; DNA synthesis;

KW replication competent double-stranded polynucleotide; ss.

XX

OS Synthetic.

OS

PN WO9914318-A1.

XX

PD 25-MAR-1999.

XX

PF 16-SEP-1998; 98WO-US19312.

XX

PR 16-SEP-1997; 97US-0059017.

XX

XX (TEXA ) UNIV TEXAS SYSTEM.

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XX Evans GA;

XX

XX WPI; 1999-244029/20.

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CC phenotypic traits (e.g. plant growth rate or crop yield), and the  
 CC segments are useful to determine the presence/absence of specific  
 CC polymorphisms correlating with the existence/absence of particular  
 CC traits. The segments are also useful in marker assisted back-cross  
 CC techniques to select plants with a higher percentage of recurrent parent  
 CC in a back-cross population. Segments incorporate SNPs which occur more  
 CC frequently than other polymorphism types and are therefore more likely  
 CC to be located close to genetic loci of interest; different forms of  
 CC characterised SNPs are also often easier to detect than other  
 CC polymorphism types.

XX  
 SQ Sequence 41 BP; 8 A; 9 C; 10 G; 13 T; 1 other;

Query Match 67.0%; Score 13.4; DB 19; Length 41;

Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 accagatggtcattc 20

|||||||

Db 40 ACGAGATGTCATTC 26

RESULT 13

AAZ55314/c

ID AAZ55314 standard; DNA; 33 BP.

XX

AC AAZ55314;

XX

DT 21-MAR-2000 (first entry)

XX

DE Neisseria species ORF cloning PCR primer #699.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;

KW antibacterial; gene therapy; PCR primer; ss.

XX

OS Synthetic.

OS Neisseria sp.

PN WO9957280-A2.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1999; 99WO-US09346.

XX

PR 01-MAY-1998; 98US-0083758.

PR

PR 31-JUL-1998; 98US-0094869.

PR

PR 02-SEP-1998; 98US-0098994.

PR

PR 02-SEP-1998; 98US-0099062.

PR

PR 09-OCT-1998; 98US-0103749.

PR

PR 09-OCT-1998; 98US-0103794.

PR

PR 09-OCT-1998; 98US-0103796.

PR

PR 25-FEB-1999; 99US-0121528.

XX

XX

PA (CHIR ) CHIRON CORP.

PA

PA (GENO-) INST GENOMIC RES.

XX

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX

DR WPI; 2000-062150/05.

XX

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CC phenotypic traits (e.g. plant growth rate or crop yield), and the  
 CC segments are useful to determine the presence/absence of specific  
 CC polymorphisms correlating with the existence/absence of particular  
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 CC in a back-cross population. Segments incorporate SNPs which occur more  
 CC frequently than other polymorphism types and are therefore more likely  
 CC to be located close to genetic loci of interest; different forms of  
 CC characterised SNPs are also often easier to detect than other  
 CC polymorphism types.

XX  
 SQ Sequence 41 BP; 8 A; 9 C; 10 G; 13 T; 1 other;

Query Match 67.0%; Score 13.4; DB 19; Length 41;

Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 accagatggtcattc 20

|||||||

Db 40 ACGAGATGTCATTC 26

RESULT 13

AAZ55314/c

ID AAZ55314 standard; DNA; 33 BP.

XX

AC AAZ55314;

XX

DT 21-MAR-2000 (first entry)

XX

DE Neisseria species ORF cloning PCR primer #699.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;

KW antibacterial; gene therapy; PCR primer; ss.

XX

OS Synthetic.

OS Neisseria sp.

PN WO9957280-A2.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1999; 99WO-US09346.

XX

PR 01-MAY-1998; 98US-0083758.

PR

PR 31-JUL-1998; 98US-0094869.

PR

PR 02-SEP-1998; 98US-0098994.

PR

PR 02-SEP-1998; 98US-0099062.

PR

PR 09-OCT-1998; 98US-0103749.

PR

PR 09-OCT-1998; 98US-0103794.

PR

PR 09-OCT-1998; 98US-0103796.

PR

PR 25-FEB-1999; 99US-0121528.

XX

XX

PA (CHIR ) CHIRON CORP.

PA

PA (GENO-) INST GENOMIC RES.

XX

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX

DR WPI; 2000-062150/05.

XX

XX

XX

XX

XX

XX

CC phenotypic traits (e.g. plant growth rate or crop yield), and the  
 CC segments are useful to determine the presence/absence of specific  
 CC polymorphisms correlating with the existence/absence of particular  
 CC traits. The segments are also useful in marker assisted back-cross  
 CC techniques to select plants with a higher percentage of recurrent parent  
 CC in a back-cross population. Segments incorporate SNPs which occur more  
 CC frequently than other polymorphism types and are therefore more likely  
 CC to be located close to genetic loci of interest; different forms of  
 CC characterised SNPs are also often easier to detect than other  
 CC polymorphism types.

XX  
 SQ Sequence 41 BP; 8 A; 9 C; 10 G; 13 T; 1 other;

Query Match 67.0%; Score 13.4; DB 19; Length 41;

CC enolase or pyruvate kinase. They can also be used for the preparation  
XX of viral particles, artificial genomes and artificial genetic systems.

SQ Sequence 50 BP; 21 A; 9 C; 8 G; 12 T; 0 other;

Query Match 66.0%; Score 13.2; DB 20; Length 50;  
Best Local Similarity 83.3%; Pred. NO. 8.9e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tttaaccagatggtcat 18  
||||| ||||| |||  
Db 14 ttctaccagatgataat 31

## RESULT 15

AAV28114  
ID AAV28114 standard; DNA; 25 BP.

XX AC

XX AAV28114;

XX 26-OCT-1998 (first entry)

XX DE Rat 5-oxoprolinase PCR primer.

XX KW 5-oxoprolinase; rat; glutathione; 5-oxoprolinuria; gene therapy;  
diagnosis; PCR; primer; ss.

XX OS Synthetic.

XX OS Rattus sp.

XX PN WO9825945-A1.

XX PD 18-JUN-1998.

XX PF 04-DEC-1997; 97WO-US22851.

XX PR 09-DEC-1996; 96US-0762428.

XX PA (CORR ) CORNELL RES FOUND INC.

XX PI Breslow E, Meister A, Ye G;

XX DR WPI; 1998-348440/30.

XX Mammalian 5-oxoprolinase - useful for developing products for  
treating 5-oxoprolinuria

XX PS Disclosure; Page 32; 66pp; English.

XX This PCR primer was used in the amplification of 5-oxoprolinase  
cDNA (see also AAV28111-12) from rat kidney cDNA. The primer  
incorporates an NdeI site at the start codon of the 5-oxoprolinase  
cDNA. The PCR product was used in the construction of expression  
plasmids for 5-oxoprolinase. Mammalian 5-oxoprolinase (m5OP)  
catalyzes the ATP dependent cleavage of 5-oxoprolinase to L-glutamate  
in the metabolism of glutathione. Deficiency of the enzyme is  
associated with 5-oxoprolinuria. The invention is directed toward  
isolated nucleic acid molecules encoding m5OP. Expression vectors  
and host cells are provided, as well as methods of increasing (by  
gene therapy) or decreasing (e.g. using antisense or ribozyme  
molecules) the expression of m5OP in host cells.

SQ Sequence 25 BP; 6 A; 9 C; 5 G; 5 T; 0 other;

Query Match 64.0%; Score 12.8; DB 19; Length 25;

Best Local Similarity 87.5%; Pred. NO. 1.3e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 tttaaccagatggtca 17

||||| ||||| |||

Db 8 tttaaccatattggcca 23

Search completed: October 2, 2001, 16:18:45  
Job time: 15489 sec





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:51 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-17

Perfect score: 20

Sequence: 1 attctcgtcgtgtgga 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-17
c 2	15.2	76.0	40	1	US-08-040-548-52
c 3	15.2	76.0	40	1	US-08-466-344-52
4	15	75.0	15	3	US-09-377-310-37
5	14.8	74.0	32	4	US-08-686-968C-20
c 6	14.2	71.0	20	2	US-08-628-422-16
c 7	13.4	67.0	18	2	US-08-313-185-16
c 8	13.4	67.0	18	3	US-09-082-614A-16
c 9	13.4	67.0	26	2	US-08-861-450-2
10	12.8	64.0	21	1	US-08-647-351B-3
c 11	12.6	63.0	30	3	US-09-392-580-43
c 12	12.6	63.0	30	1	US-08-295-670-3
c 13	12.6	63.0	30	1	US-08-633-485-3
14	12.2	61.0	20	1	US-08-202-042-4
15	12.2	61.0	21	4	US-08-430-225A-13
16	12.2	61.0	24	1	US-07-923-724-12
17	12.2	61.0	24	2	US-08-609-426A-12
c 18	12.2	61.0	29	1	US-07-642-734C-19
c 19	12.2	61.0	29	3	US-08-439-009A-19
c 20	12.2	61.0	31	3	US-09-123-764-5
c 21	12.2	61.0	31	5	PCT-US94-07091-1
22	12.2	61.0	38	3	US-08-938-830-19
23	12.2	61.0	38	3	US-09-020-222-19
24	12.2	61.0	39	4	US-08-993-674A-66
c 25	12.2	61.0	42	2	US-08-124-981A-18
c 26	12.2	61.0	42	3	US-09-037-190-16
c 27	12.2	61.0	42	3	US-09-037-192-16

c 28	12.2	61.0	42	3	US-09-037-143-16	Sequence 16, Appl
c 29	12.2	61.0	42	4	US-09-049-691-16	Sequence 16, Appl
c 30	12.2	61.0	42	4	US-08-260-174-16	Sequence 16, Appl
c 31	12.2	61.0	49	4	US-08-993-674A-67	Sequence 67, Appl
c 32	12	60.0	27	2	US-08-859-998-1095	Sequence 1095, Ap
c 33	12	60.0	28	1	US-08-558-719-2	Sequence 2, Appli
c 34	12	60.0	28	2	US-08-558-651-2	Sequence 2, Appli
c 35	12	60.0	31	1	US-07-866-560-2	Sequence 2, Appli
c 36	12	60.0	31	1	US-07-866-979-2	Sequence 2, Appli
c 37	12	60.0	31	1	US-08-077-673-2	Sequence 2, Appli
c 38	12	60.0	31	1	US-08-478-992-2	Sequence 2, Appli
c 39	12	60.0	31	3	US-09-105-298-2	Sequence 2, Appli
c 40	12	60.0	33	4	US-09-232-468A-38	Sequence 38, Appl
c 41	12	60.0	45	1	US-08-067-160-19	Sequence 19, Appl
c 42	12	60.0	45	2	US-08-717-394-19	Sequence 19, Appl
c 43	12	60.0	45	2	US-08-487-110-19	Sequence 19, Appl
c 44	12	60.0	45	3	US-09-028-648A-19	Sequence 19, Appl
c 45	12	60.0	45	3	US-09-028-587-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-09-377-310-17  
; Sequence 17, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Antisense Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-17

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtgtgga 20  
Db 1 attctcgtcgtgtgga 20

RESULT 2  
US-08-040-548-52/c  
; Sequence 52, Application US/08040548  
; Patent No. 5763209  
; GENERAL INFORMATION:  
; APPLICANT: Sukhatme, Vikas P.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5763209th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,548  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-040-548-52

Query Match 76.0%; Score 15.2; DB 1; Length 40;  
Best Local Similarity 85.0%; Pred. No. 72;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtgaa 20  
||||| ||||| |||||  
Db 21 ATTCTCGTGTCTGCCGAA 2

RESULT 3  
US-08-466-344-52/c  
Sequence 52, Application US/08466344  
Patent No. 5773583  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5773583th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,344  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/040,548  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-466-344-52

Query Match 76.0%; Score 15.2; DB 1; Length 40;  
Best Local Similarity 85.0%; Pred. No. 72;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtgaa 20  
||||| ||||| |||||  
Db 21 ATTCTCGTGTCTGCCGAA 2

RESULT 4  
US-09-377-310-37  
Sequence 37, Application US/09377310B  
Patent No. 6133031  
GENERAL INFORMATION:  
APPLICANT: Monia, Brett P.  
APPLICANT: Gaarde, William A.  
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
TITLE OF INVENTION: Expression  
FILE REFERENCE: ISPH-0389  
CURRENT APPLICATION NUMBER: US/09/377,310B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 37  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: antisense sequence  
US-09-377-310-37

Query Match 75.0%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tctctcgtcgtcgtggtg 17  
||||| ||||| |||||  
Db 1 tctctcgtcgtcgtggtg 15

RESULT 5  
US-08-686-968C-20  
Sequence 20, Application US/08686968C  
Patent No. 6221361  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
FILE REFERENCE: 39119-H/JML  
CURRENT APPLICATION NUMBER: US/08/686,968C  
CURRENT FILING DATE: 1996-07-25  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 20  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-686-968C-20

Query Match 74.0%; Score 14.8; DB 4; Length 32;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtg 18

```
Db 15 attctgctgagtgtg 32
||||| ||||| |||||
RESULT 6
US-08-628-422-16/c
; Sequence 16, Application US/08628422
; Patent No. 5837854
; GENERAL INFORMATION:
; APPLICANT: Mulder, Carel
; TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-BARR
; TITLE OF INVENTION: VIRUS ACTIVITY
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/628,422
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/094001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-628-422-16

Query Match 71.0%; Score 14.2; DB 2; Length 20;
Best Local Similarity 84.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ttctcgtcgtcgtgga 20
||||| ||||| |||||
Db 20 TTGCTCGAGCTGGAGAA 2

RESULT 7
US-08-313-185-16/c
; Sequence 16, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
```

```
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-16

Query Match 67.0%; Score 13.4; DB 2; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ctcgctgctggtgga 19
||||| ||||| |||||
Db 16 CTCGCTGGGTGGA 2

RESULT 8
US-09-082-614A-16/c
; Sequence 16, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356-0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-082-614A-16

Query Match 67.0%; Score 13.4; DB 3; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ctcgctgctggtgga 19
Db 16 CTCGCTGCGGTGGA 2

RESULT 9
US-08-861-450-2/c
; Sequence 2, Application US/08861450
; Patent No. 5908764
; GENERAL INFORMATION:
; APPLICANT: Br nker, Peter
; APPLICANT: Minas, Wolfgang
; APPLICANT: Kallio, Pauli
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: INCREASING PRODUCTION OF ERYTHROMYCIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,450
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 9092-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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```
; TOPOLOGY: linear
; US-08-861-450-2

Query Match 67.0%; Score 13.4; DB 2; Length 26;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 tcgctgctggtgga 20
Db 26 TAGCTGCTGCTGGAA 12

RESULT 10
US-08-647-351B-3
; Sequence 3, Application US/08647351B
; Patent No. 5770368
; GENERAL INFORMATION:
; APPLICANT: De Leon, Ricardo
; APPLICANT: Rochelle, Paul
; TITLE OF INVENTION: Cryptosporidium Detection Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 S. Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: California
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,351B
; FILING DATE: May 9, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farah, David A.
; REGISTRATION NUMBER: 38,134
; REFERENCE/DOCKET NUMBER: 11364
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: primer sequence
; US-08-647-351B-3

Query Match 64.0%; Score 12.8; DB 1; Length 21;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ctcgctgctggtgga 20
Db 4 CTTGCTGCTGCTGGAA 19

RESULT 11
US-09-392-580-43/c
; Sequence 43, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRES
```

FILE REFERENCE: RTS-0072  
CURRENT APPLICATION NUMBER: US/09/392,580  
CURRENT FILING DATE: 1999-09-09  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 43  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-392-580-43

Query Match 63.0%; Score 12.6; DB 3; Length 20;  
Best Local Similarity 78.9%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 attctcgtcgtcgtgga 19  
Db 19 ATTGTTCCATGCTGCTGGA 1

RESULT 12  
US-08-295-670-3  
Sequence 3, Application US/08295670  
Patent No. 5547864  
GENERAL INFORMATION:  
APPLICANT: KAWASAKI, HISASHI  
APPLICANT: TSUCHIYA, MAKOTO  
APPLICANT: MIWA, KIYOSHI  
APPLICANT: KAWAHARA, YOSHIO  
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,670  
FILING DATE: 08-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/00039  
FILING DATE: 13-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-4069  
FILING DATE: 13-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5547864man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-697-0 PCT  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-295-670-3

Query Match 63.0%; Score 12.6; DB 1; Length 30;  
Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 ttctcgtcgtcgtggtgaa 20  
Db 1 TTCATCGCTGCTGCTCGGCA 19

RESULT 13  
US-08-633-485-3  
Sequence 3, Application US/08633485  
Patent No. 5681717  
GENERAL INFORMATION:  
APPLICANT: KAWASAKI, HISASHI  
APPLICANT: TSUCHIYA, MAKOTO  
APPLICANT: MIWA, KIYOSHI  
APPLICANT: KAWAHARA, YOSHIO  
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,485  
FILING DATE: 17-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/295,670  
FILING DATE: 08-SEP-1994  
APPLICATION NUMBER: PCT/JP94/00039  
FILING DATE: 13-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-4069  
FILING DATE: 13-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5681717man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-697-0 PCT  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-633-485-3

Query Match 63.0%; Score 12.6; DB 1; Length 30;  
Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 ttctcgtcgtcgtggtgaa 20  
Db 1 TTCATCGCTGCTGCTCGGCA 19

RESULT 14  
US-08-202-042-4  
; Sequence 4, Application US/08202042  
; Patent No. 5686072  
; GENERAL INFORMATION:  
; APPLICANT: Jonathan W. Uhr  
; APPLICANT: Ellen S. Vitetta  
; TITLE OF INVENTION: EPITOPE-SPECIFIC MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES AND IMMUNOTOXINS  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/202,042  
; FILING DATE: Submitted herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David L. Parker  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:379/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 320-7200  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: oligonucleotide  
US-08-202-042-4

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Best Local Similarity 82.4%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtg 17  
||| ||||| |||||  
Db 4 ATTCTCGCTCGTGTG 20

RESULT 15  
US-08-430-225A-13  
; Sequence 13, Application US/08430225A  
; Patent No. 6204000  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Jin-Tang; Barrett,  
; APPLICANT: J. Carl; Patricia W.; Isaacs, John T.  
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND  
; TITLE OF INVENTION: GENE THERAPY USING REAGENTS DERIVED FROM THE  
; TITLE OF INVENTION: HUMAN METASTASIS SUPPRESSOR GENE KAI1  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,225A  
; FILING DATE: 28-APR-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RICHARD W. BORK  
; REGISTRATION NUMBER: 36,459  
; REFERENCE/DOCKET NUMBER: 2026-4172  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; TELEX: 421792  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-430-225A-13

Query Match 61.0%; Score 12.2; DB 4; Length 21;  
Best Local Similarity 82.4%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtg 17  
||| ||||| ||||| ||  
Db 1 AGTCTCGCTCGTGTG 17

Search completed: October 2, 2001, 16:03:52  
Job time: 14596 sec





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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:44 ; Search time 876.95 Seconds  
(without alignments)  
14.320 Million cell updates/sec

Title: US-09-757-100b-17

Perfect score: 20

Sequence: 1 attctcgtcgtggtgaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	Human focal adhesi
2	15	75.0	15	22	Human focal adhesi
3	14.8	74.0	32	19	IBRV gi gene PCR p
4	14.8	74.0	35	21	3' oligonucleotide
5	14.2	71.0	20	18	BZLF1 gene specifi
6	14	70.0	18	14	Primer pair #6 Oli
7	14	70.0	18	14	PCR primer used to
8	13.6	68.0	32	15	BoPCar I, bovine p
9	13.4	67.0	20	20	PCR primer used to
10	13.4	67.0	26	20	PmerR promoter amp
11	13.2	66.0	20	19	Human biallelic po

C 12	13	65.0	23	21	AAC87185	Rice mutant BPSPS
C 13	13	65.0	23	21	AAC88395	Primer Universal r
C 14	13	65.0	23	21	AAC89319	Primer Universal r
C 15	12.8	64.0	19	21	AAA82953	cdk6 ribozyme bind
C 16	12.8	64.0	21	18	AAT89992	Cryptosporidium he
C 17	12.6	63.0	20	20	AAX97166	Primer used to amp
C 18	12.6	63.0	20	21	AAA64943	Antisense oligonuc
C 19	12.6	63.0	30	15	AAQ70365	B.lactofermentum c
C 20	12.4	62.0	18	14	AAQ37914	Beta-casein sequen
C 21	12.4	62.0	18	17	AAQ27829	Primer #1 for mali
C 22	12.4	62.0	21	21	AAA48928	Reverse primer PB.
C 23	12.4	62.0	29	21	AAF05016	Hammerhead ribozym
C 24	12.4	62.0	31	20	AAX02733	Eubacterial 16S rR
C 25	12.4	62.0	31	21	AAZ45459	Primer O265 used t
C 26	12.4	62.0	38	21	AAC69811	E. coli O356 SELEX
C 27	12.2	61.0	20	13	AAT93237	Antisense oligonuc
C 28	12.2	61.0	20	20	AAQ04613	PCR primer used to
C 29	12.2	61.0	21	17	AAT40022	Primer for human K
C 30	12.2	61.0	21	19	AAV57633	Exon 1 of an ENAC
C 31	12.2	61.0	24	15	AAQ58130	cbhl-Phytase prime
C 32	12.2	61.0	29	14	AAQ46797	pAeryAKS2 primer
C 33	12.2	61.0	30	20	AAQ16994	A. thaliana endo-1
C 34	12.2	61.0	31	16	AAQ76298	Staphylococcus aur
C 35	12.2	61.0	31	18	AAQ62574	Granule bound star
C 36	12.2	61.0	31	21	AAA79051	Human genomic DNA
C 37	12.2	61.0	37	9	AAH81428	Sequence of synthe
C 38	12.2	61.0	38	19	AAV57997	Murine PSTPIP PCR
C 39	12.2	61.0	38	21	AAQ64251	PCR primer for PTP
C 40	12.2	61.0	38	21	AAQ07288	PCR primer for PS
C 41	12.2	61.0	41	21	AAQ73359	Single base extens
C 42	12.2	61.0	42	16	AAQ86682	NF-AT transcrip tio
C 43	12.2	61.0	42	21	AAQ09113	PCR Primer KXF to
C 44	12.2	61.0	42	21	AAQ29268	Human nuclear fact
C 45	12.2	61.0	42	22	AAQ31700	Human NF-AT polynu

#### ALIGNMENTS

RESULT 1	
AAC65549	AAC65549 standard; DNA; 20 BP.
ID	AC
AC	AAC65549;
DF	12-FEB-2001 (first entry)
DE	Human focal adhesion kinase antisense sequence #15.
XX	Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW	embryonic development disorder; angiogenic disorder; wound healing;
KW	antisense; phosphorothioate; ss.
XX	Homo sapiens.
XX	US6133031-A.
XX	17-OCT-2000.
XX	19-AUG-1999; 99US-0377310.
XX	19-AUG-1999; 99US-0377310.
XX	(ISIS-) ISIS PHARM INC.
XX	Monia BP, Gaarde WA;
XX	WPI; 2001-006141/01.
XX	New antisense compounds for inhibiting focal adhesion kinase
PT	expression, especially useful for inhibiting retinal
PT	neovascularization, or for diagnosing and treating e.g. colon cancer -
XX	

PS Example 2; Column 23; 30pp; English.

CC The present invention describes a number of phosphorothioate antisense  
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
 CC is involved in integrin-mediated signal transduction, and is implicated  
 CC in cancer, particularly colon, breast and oral tumours, embryonic  
 CC development disorders, angiogenic disorders and wound healing. The  
 CC antisense sequences, including the one shown here, can be used in the  
 CC treatment of all of these.

XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20

|||||

Db 1 attctcgtcgtggtgaa 20

RESULT 2

AAC65569

ID AAC65569 standard; DNA; 15 BP.

AC AAC65569;

XX 12-FEB-2001 (first entry)

DE Human focal adhesion kinase antisense sequence #35.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

OS Homo sapiens.

PN US6133031-A.

PD 17-OCT-2000.

XX 19-AUG-1999; 99US-0377310.

XX 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Monla BP, Gaarde WA;

PI WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase  
 PT expression, especially useful for inhibiting retinal  
 PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX Example 2; Column 25; 30pp; English.

PS The present invention describes a number of phosphorothioate antisense  
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
 CC is involved in integrin-mediated signal transduction, and is implicated  
 CC in cancer, particularly colon, breast and oral tumours, embryonic  
 CC development disorders, angiogenic disorders and wound healing. The  
 CC antisense sequences, including the one shown here, can be used in the  
 CC treatment of all of these.

XX Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 other;

Query Match

Best Local Similarity 75.0%; Score 15; DB 22; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tctcgtcgtcgtggtg 17

|||||

Db 1 tctcgtcgtcgtggtg 15

RESULT 3

AAV26137

ID AAV26137 standard; DNA; 32 BP.

XX AAV26137;

XX 24-JUL-1998 (first entry)

DE IBRV gI gene PCR primer SEQ ID NO:20 from WO9804684 Example 41.

XX Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;  
 KW pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;  
 KW Dirofilaria immitis; PCR primer; ss.

XX Synthetic.

XX WO9804684-A1.

XX 05-FEB-1998.

XX 25-JUL-1997; 97WO-US12212.

XX 25-JUL-1996; 96US-0686968.

XX (SYTR ) SYNTRO CORP.

XX Cochran MD, Junker DE;

XX WPI; 1998-130677/12.

XX Recombinant swine pox virus - useful in vaccine for immunising  
 PT animal against swine pox virus  
 PT Example 41; Page 180; 473pp; English.

XX The present sequence represents a PCR primer used in an example from the  
 CC present invention. The present invention specifically describes  
 CC recombinant swinepox virus (SPV) comprising a foreign DNA (I) inserted  
 CC into a SPV genome which is capable of being expressed in a host cell  
 CC into which the virus is introduced, where (I) is inserted into: (a) an  
 CC EcoRI site within a region corresponding to a 3.2 kb subfragment of the  
 CC HindIII K fragment which contains both a HindIII and an EcoRI site, of  
 CC the SPV genome, and optionally (b) an AccI site within a region  
 CC corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M  
 CC fragment. The recombinant SPV can be used in a vaccine for immunising an  
 CC animal against SPV. The invention also provides a method for testing a  
 CC swine to determine whether the swine has been vaccinated with a  
 CC vaccine, particularly containing S-SPV-008, or is infected with a  
 CC naturally occurring wild-type pseudorabies virus. Also (I) inserted into  
 CC recombinant SPV can be used in a diagnostic assay, e.g. Feline  
 CC immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis  
 CC p39 and 22kd are useful to detect feline immunodeficiency caused by FIV  
 CC and to detect heartworm caused by D. immitis respectively.

XX Sequence 32 BP; 4 A; 7 C; 10 G; 11 T; 0 other;

Query Match

Best Local Similarity 74.0%; Score 14.8; DB 19; Length 32;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtg 18

|||||

Db 15 attctcgtcgtggtg 32

RESULT 4

AAA70370

ID AAA70370 standard; DNA; 35 BP.  
 AC AAA70370;  
 XX  
 DT 02-FEB-2001 (first entry)  
 XX  
 DE 3' oligonucleotide # 1 used for cloning human placental bikunin cDNA.  
 XX  
 KW Mucociliary dysfunction; mucus; sputum; human;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200037099-A2.  
 PN  
 XX 29-JUN-2000.  
 PD  
 XX 22-DEC-1999; 99WO-GB04381.  
 XX  
 XX 22-DEC-1998; 98US-0218913.  
 PR  
 PR 17-NOV-1999; 99US-0441966.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 XX Hall R, Poll CT, Newton BB, Taylor WJA;  
 PI  
 XX WPI: 2000-452127/39.  
 DR  
 XX Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PT always for treating lung diseases such as cystic fibrosis and  
 PT bronchitis involves administering a Kunitz-type serine protease  
 PT inhibitor  
 XX  
 XX Example 6; Page 52; 173pp; English.  
 PS  
 XX Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
 CC complication of chronic obstructive lung diseases such as Chronic  
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. A partial coding sequence  
 CC for human placental bikunin has been isolated (see AAA70371). Placental  
 CC bikunin is a Kunitz-type serine protease inhibitor protein, which can  
 CC stimulate the rate of mucociliary clearance of mucus and sputum in lung  
 CC airways. Therefore, placental bikunin protein may be used for treating  
 CC lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear  
 CC which are caused by retention and accumulation of mucus. The present  
 CC sequence is an oligonucleotide used to clone the partial human placental  
 CC bikunin coding sequence of AAA70371.  
 XX  
 SQ Sequence 35 BP; 7 A; 9 C; 14 G; 5 T; 0 other;

Query Match 74.0%; Score 14.8; DB 21; Length 35;  
 Best Local Similarity 88.9%; Pred. No. 3.9e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 tcctcgtctgctggtggaa 20  
 ||||| ||||| |||||  
 Db 6 tcctcactgctgctggtggaa 23

RESULT 5  
 AAT92645/c  
 ID AAT92645 standard; DNA; 20 BP.  
 XX  
 XX AAT92645;  
 AC  
 XX 22-APR-1998 (first entry)  
 DT  
 XX B2LF1 gene specific antisense oligonucleotide 212.

XX Epstein-Barr virus; antisense oligonucleotide; EBV; treatment; tumour;  
 KW B2LF1; BRLF1; BMLF1; BLRF1; BHRF1; BYRF1; BSLF2; BSLF2; ss.  
 XX  
 OS Synthetic.  
 OS Epstein-Barr virus.  
 PN WO9737669-A1.  
 XX  
 XX 16-OCT-1997.  
 PD  
 XX 04-APR-1997; 97WO-US06104.  
 PF  
 XX 05-APR-1996; 96US-0628422.  
 PR  
 XX (UYMA-) UNIV MASSACHUSETTS.  
 PA  
 XX Mulder C;  
 PI  
 XX WPI: 1997-512403/47.  
 DR  
 XX Anti-sense oligo:nucleotide(s) that inhibit Epstein-Barr virus  
 PT function - used to treat or prevent EB virus infections, including  
 PT tumours  
 PT  
 XX Claim 5; Page 54; 79pp; English.  
 PS  
 XX This antisense oligonucleotide is specific to a portion of the B2LF1  
 CC gene. Antisense oligonucleotides specific to any of the different  
 CC strains of Epstein-Barr virus (EBV) such as the B2LF1, BRLF1, BMLF1,  
 CC B1LF1, BNLF1, BYRF1, BHRF1, BSLF2 and terminal proteins 1 and 2  
 CC are used to inhibit EBV function. These antisense oligonucleotides are  
 CC antisense sequences that inhibit EBV replication or gene expression. The  
 CC antisense oligonucleotides or the vectors expressing them, are used to  
 CC treat or prevent EBV infection (including tumours such as nasopharyngeal  
 CC carcinoma) in mammals. When labelled, they can also be used to detect  
 CC cells infected with EBV. The antisense oligonucleotides can be targeted  
 CC to either the latent or the lytic phase of the virus cycle. Combinations  
 CC of the antisense oligonucleotides directed against different viral genes  
 CC may provide a synergistic inhibitory effect. Formulation of these  
 CC antisense oligonucleotides with transfection agents can increase the  
 CC efficiency and reduce their needed dosage.  
 XX  
 SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match 71.0%; Score 14.2; DB 18; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 7.1e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 ttctcgtctgctggtggaa 20  
 ||||| ||||| |||||  
 Db 20 TTGCTCGCAGCTGGAGGAA 2

RESULT 6  
 AAQ61472/c  
 ID AAQ61472 standard; DNA; 18 BP.  
 XX  
 AC AAQ61472;  
 XX  
 XX 17-MAY-1994 (first entry)  
 DT  
 XX Primer pair #6 Oligo2 to amplify M.tuberculosis katG gene.  
 DE  
 XX catalase-peroxidase; isonicotinic acid hydrazide; isoniazid; INH;  
 KW antibiotic; susceptibility; sensitive; resistant; katG;  
 KW polymerase chain reaction; Single strand conformation polymorphism;  
 KW PCR-SSCP analysis; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH

```

FT misc_difference 8
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FT FT /note= "letter O printed at this site in the
FT FT specification"
XX
XX WO9322454-A.
XX
XX 11-NOV-1993.
XX
XX 30-APR-1993; 93WO-EP01063.
XX
XX 17-SEP-1992; 92FR-0011098.
XX 30-APR-1992; 92US-0875940.
XX 14-AUG-1992; 92US-0929206.
XX 16-APR-1993; 93FR-0004545.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE.
XX (INSP) INST PASTEUR.
XX (MEDI-) MEDICAL RES COUNCIL.
XX (UYBE-) UNIV BERNE.
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Bodmer T, Cole S, Heym B, Honore N, Telenti A;
XX Young D, Zhang Y;
XX
XX WPI; 1993-368812/46.
XX
XX Rapid detection of antibiotic resistance in Mycobacteria - esp.
XX isoniazid, rifampicin or streptomycin resistance in tuberculosis
XX by detecting mutation in katG, rpoB or rpsL genes
XX
XX Example 2; Page 29; 97pp; English.
XX
XX Eleven pairs of primers were synthesised and used to generate PCR
XX products of around 280bp, that covered the complete katG gene and
XX some of the flanking sequences. With these primers, a panel of
XX INH-resistant strains of M.tuberculosis was examined using PCR-SSCP
XX analysis to localise the katG mutations responsible for isoniazid
XX resistance.
XX
XX Sequence 18 BP; 5 A; 6 C; 5 G; 1 T; 1 other;

Query Match 70.0%; Score 14; DB 14; Length 18;
Best Local Similarity 93.3%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ctcgctgctgtgga 19
DB 16 CTCGCTGCNGGTGA 2

RESULT 7
ID AAA58527/c
XX AAA58527 standard; DNA; 18 BP.
XX
XX AAA58527;
XX
XX 20-OCT-2000 (first entry)
XX
XX PCR primer used to amplify bleomycin (BLM) gene cluster ORF34.
XX
XX BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
XX bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
XX thiazoline; bithiazoline; microbial metabolite; sugar; PCR primer; ss.
XX
XX Streptomyces verticillus.
XX
XX WO200040704-A1.
XX
XX 13-JUL-2000.
XX
XX 06-JAN-2000; 2000WO-US00445.

XX
XX 06-JAN-1999; 99US-0115435.
XX 05-FEB-1999; 99US-0118848.
XX 05-JAN-2000; 2000US-0477962.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Shen B, Du L, Sanchez C, Chen M, Edwards DJ;
XX
XX WPI; 2000-465974/40.
XX
XX New bleomycin gene cluster components useful for peptide and/or
XX polyketide metabolites, especially bleomycin, production and for
XX chemically modifying biological molecules -
XX
XX Disclosure; Page 22; 162pp; English.
XX
XX PCR primers AAA58474-A58541 were used to amplify open reading frames
XX (ORFs) 8 to 41 of the BLM (Bleomycin) gene cluster. The proteins encoded
XX by the gene cluster are useful for producing peptides and/or polyketide
XX metabolites, especially bleomycin or bleomycin analogues. They are
XX also useful for chemically modifying biological molecules to produce
XX branched methyl groups, and for coupling amino acids and fatty
XX acids. They may be reacted with an apo-carrier protein and coenzyme A
XX to produce a holo-carrier protein. The BLM gene cluster or catalytic
XX domains can be used individually or collectively to produce
XX thiazolidine, thiazoline, bithiazoline and bithiazoline-containing
XX microbial metabolites. The BLM gene cluster may also be used to produce
XX sugars.
XX
XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 other;

Query Match 70.0%; Score 14; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ctcgctgctgtggtg 17
DB 17 CCTCGCTGCTGGTG 4

RESULT 8
ID AAQ88809
XX AAQ88809 standard; cDNA to mRNA; 32 BP.
XX
XX AAQ88809;
XX
XX 27-APR-1995 (first entry)
XX
XX BoPCar I, bovine parathyroid calcium receptor PCR primer.
XX
XX BoPCar I; bovine parathyroid calcium receptor; hyperparathyroidism;
XX ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 8
XX /tag= a
XX /mod_base= i
XX modified_base 13
XX /tag= b
XX /mod_base= i
XX
XX WO9418959-A.
XX
XX 01-SEP-1994.
XX
XX 23-FEB-1993; 93WO-US01642.
XX
XX 23-FEB-1993; 93AU-0037770.
XX 23-FEB-1993; 93WO-US01642.

```

XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 PA (NPSP-) NPS PHARM INC.  
 PI Balandrin MF, Brown EM, Del MAR EG, Fuller FH, Hebert SC;  
 PI Nemeth EF, Van WAGENEN BC;  
 XX WPI; 1994-293958/36.  
 XX Compn. contg. partly new calci-mimetic and calcilytic cpds. -  
 PT for treating parathyroidism, Paget's disease etc. and for  
 PT diagnosis, also new ion receptors and associated nucleic acid,  
 PT antibodies and transgenic animals  
 XX Disclosure; Page 100; 283pp; English.  
 XX  
 XX AAQ88809 was used in combination with AAQ88810 as primers for the  
 CC PCR amplification of BopCAR 1, bovine parathyroid  
 CC calcium receptor, which was used to test the effectiveness of  
 CC new calci-mimetics that mimics the action of extracellular  
 CC Ca ions. These calci-mimetics can be used in the treatment  
 CC of a variety of diseases associated with abnormal levels of  
 CC Ca in cells, blood and plasma, specifically hyperparathyroidism.  
 XX Sequence 32 BP; 5 A; 4 C; 8 G; 8 T; 7 other;  
 SQ

Query Match 68.0%; Score 13.6; DB 15; Length 32;  
 Best Local Similarity 70.0%; Pred. No. 1.4e+03;  
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20  
 | | | | | : | | | | |  
 Db 5 actnctgntbctgtgtggar 24

RESULT 9  
 AAX96509/c  
 ID AAX96509 standard; DNA; 20 BP.  
 XX  
 AC AAX96509;  
 XX  
 DT 13-SEP-1999 (first entry)  
 XX  
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.  
 XX  
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;  
 KW vaccine; neutralising epitope; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Chlamydia pneumoniae.  
 XX  
 PN WO927105-A2.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 20-NOV-1998; 98WO-IB01890.  
 XX  
 PR 04-NOV-1998; 98US-0107078.  
 PR 21-NOV-1997; 97FR-0014673.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Griffais R;  
 XX  
 DR WPI; 1999-357842/30.  
 XX  
 XX Genome sequence of Chlamydia pneumoniae  
 PT  
 PS Page 1831; Disclosure; 1912pp; English.  
 XX  
 XX AAX91991-X97517 represent PCR primers used to amplify open reading

CC frames and other nucleic acid sequences from the genome of  
 CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory  
 CC disease such as pneumonia and bronchitis and is thought to be a  
 CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent  
 CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded  
 CC by the open reading frames of the C. pneumoniae genome (see AAY34584-  
 CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors  
 CC containing C. pneumoniae nucleotide sequences can also be used as  
 CC immunogenic compositions, especially where the vector directs the  
 CC expression of a neutralising epitope of C. pneumoniae.  
 XX  
 SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 other;  
 SQ

Query Match 67.0%; Score 13.4; DB 20; Length 20;  
 Best Local Similarity 93.3%; Pred. No. 1.7e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 attctcgtcgtgctgg 15  
 | | | | | : | | | | |  
 Db 19 ACTCCTCGCTGCTGG 5

RESULT 10  
 AAX05609/c  
 ID AAX05609 standard; DNA; 26 BP.  
 XX  
 AC AAX05609;  
 XX  
 DT 21-APR-1999 (first entry)  
 XX  
 DE PmerR promoter amplifying reverse primer.  
 XX  
 KW Erythromycin; oxygen-binding protein; transformation; S. erythraea;  
 KW PmerR promoter; Vitreoscilla; haemoglobin; Vhb; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Streptomyces sp.  
 XX  
 PN WO9853084-A1.  
 XX  
 PD 26-NOV-1998.  
 XX  
 PF 22-MAY-1998; 98WO-IB00790.  
 XX  
 PR 22-MAY-1997; 97US-0861450.  
 XX  
 PA (SOLI-) SOLIDAGO AG.  
 XX  
 PI Bailey JE, Brunner P, Kallio P, Minas W;  
 XX  
 DR WPI; 1999-070154/06.  
 XX  
 PT New organism expressing oxygen-binding protein - useful, e.g. in  
 PT methods for highly efficient production of erythromycin  
 XX  
 PS Example 1; Page 15; 44pp; English.  
 XX  
 CC The invention provides an erythromycin-producing organism that expresses  
 CC a heterologous oxygen-binding protein. The oxygen-binding protein can be  
 CC used in a method for increasing erythromycin production that comprises  
 CC culture of oxygen-binding protein under erythromycin production  
 CC conditions. The method is exemplified by stably transforming  
 CC Saccharopolyspora erythraea with an exogenous DNA construct, comprising  
 CC directing integration of the construct at the phl C31 attachment site of  
 CC the S. erythraea chromosome. The organism and the methods are used to  
 CC provide more efficient production of erythromycin. Sequences  
 CC AAX05608-609 represent PCR primers used for the amplification of PmerR  
 CC promoter. This is used in the construction of expression vectors  
 CC containing Vitreoscilla haemoglobin (Vhb) and chromosomal integration of  
 CC the Vhb expression cassette in S. erythraea.  
 XX  
 SQ Sequence 26 BP; 6 A; 9 C; 3 G; 8 T; 0 other;  
 SQ

Query Match 67.0%; Score 13.4; DB 20; Length 26;  
 Best Local Similarity 93.3%; Pred. No. 1.7e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 tcgctgctggtgga 20  
 Db 26 TAGCTGCTGGTGGAA 12

RESULT 11  
 AAX09838/c  
 ID AAX09838 standard; DNA; 20 BP.  
 XX AC AAX09838;  
 XX DT 24-MAR-1999 (first entry)  
 XX DE Human biallelic polymorphic marker downstream primer #144.  
 KW Polymorphism: biallelic; human; forensic; paternity testing; disease;  
 KW detection; phenotypic typing; characteristic; infection; hereditary;  
 KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;  
 KW treatment; marker; primer; ss.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 PN WO9820165-A2.  
 XX PD 14-MAY-1998.  
 XX PF 05-NOV-1997; 97WO-US20313.  
 XX PR 06-NOV-1996; 96US-0030455.  
 XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX PI Hudson T, Lander ES, Wang D;  
 XX WPI: 1998-286974/25.

New isolated nucleic acid segments from the human genome - used for  
 determining polymorphic forms for use in e.g. forensics, paternity  
 testing or phenotypic typing for disease

Claim 16; Page 63; 310pp; English.

AAX09121-X10268 are allele-specific oligonucleotide primers used in the  
 isolation of various biallelic polymorphic markers found in the human  
 genome (represented in AAX10269-X12937). These primers can be used in a  
 method for determining polymorphic forms in an individual for use in  
 e.g. forensics, paternity testing or for phenotypic typing for diseases  
 such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,  
 muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial  
 hypercholesterolemia, polycystic kidney disease, hereditary  
 spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary  
 haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos  
 syndrome, osteogenesis imperfecta, acute intermittent porphyria,  
 autoimmune diseases, inflammation, cancer, diseases of the nervous  
 system, infection by pathogenic microorganisms, and characteristics such  
 as longevity, appearance (e.g. baldness, obesity), strength, speed,  
 endurance, fertility, and susceptibility or receptivity to particular  
 drugs or therapeutic treatments. The isolated polymorphic nucleic acid  
 segments can also be used to produce medicaments for the treatment or  
 prophylaxis of such diseases.

Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 other;

Query Match 66.0%; Score 13.2; DB 19; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ttctcgctgctggtgga 19  
 Db 20 TTCCTCTCTTCGCGGA 3

RESULT 12  
 AAC87185/c  
 ID AAC87185 standard; DNA; 23 BP.  
 XX AC AAC87185;  
 XX DT 09-MAR-2001 (first entry)  
 XX DE Rice mutant EPSPS PCR primer, SEQ ID NO:40.  
 KW Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase;  
 KW glyphosate resistance; herbicide resistance; transgenic plant;  
 KW expression construct; PCR primer; ss.  
 XX OS Oryza sativa.  
 XX OS Synthetic.  
 PN WO200066748-A1.  
 XX PD 09-NOV-2000.  
 XX PF 20-APR-2000; 2000WO-CB01573.  
 XX PR 29-APR-1999; 99GB-0009968.  
 XX PR 29-APR-1999; 99GB-0017834.  
 XX PR 29-APR-1999; 99GB-0030213.  
 XX PR 29-JUL-1999; 99GB-0017839.  
 XX PR 29-JUL-1999; 99GB-0017840.  
 XX PR 29-JUL-1999; 99GB-0017846.  
 XX PR 29-JUL-1999; 99GB-0017847.  
 XX PR 21-DEC-1999; 99GB-0030200.  
 XX PR 21-DEC-1999; 99GB-0030204.  
 XX PR 21-DEC-1999; 99GB-0030207.  
 XX PR 21-DEC-1999; 99GB-0030209.  
 XX PA (ZENE ) ZENECA LTD.  
 XX PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;  
 XX WPI: 2000-687544/67.

Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate  
 synthase, used to produce transgenic plants e.g. banana, wheat, maize  
 or rice, having resistance or tolerance to glyphosate herbicide -

Example 20; Page 51; 87pp; English.

The invention relates to rice 5-enolpyruvylshikimate phosphate synthase  
 (EPSPS) genomic DNA (AAC87188). The invention also relates to an  
 expression cassette comprising, in the 5'-3' direction, one or more  
 transcriptional enhancer elements selected from AAC87190-C87196), the  
 rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast  
 transit peptide, genomic DNA encoding a EPSPS protein modified such that  
 it is resistant to glyphosate (AAC87189), and a transcriptional  
 terminator. The glyphosate resistant EPSPS contains a region (AAB29793)  
 containing two amino acid substitutions relative to the corresponding  
 wild-type region (AAB29792). The invention also encompasses plant genomic  
 EPSPS sequences identified via screening with a rice EPSPS intronic  
 sequence; vectors and host plant cells comprising a nucleic acid sequence  
 of the invention; transgenic plants (and tissues and seeds thereof)  
 comprising a nucleic acid sequence of the invention, optionally further  
 transformed with a DNA encoding an insect, fungal, viral, bacterial,  
 nematode, stress or herbicide resistance protein; and methods of  
 producing the transgenic plants of the invention. The nucleic acids and  
 constructs of the invention are used to produce a wide variety of  
 morphologically normal, glyphosate resistant plants. The glyphosate



CC resistant plants produced are particularly maize, soybean, cotton,  
 CC sugarbeet and canola, but also other field crops, fruits and vegetables,  
 CC turf and forage grasses and nut-producing plants. The plants are  
 CC optionally resistant to insects, fungi, viruses, bacteria, nematodes,  
 CC stress, desiccation and/or other herbicides. They can be used in the  
 CC production of a herbicidal target for the high throughput in vitro  
 CC screening of potential herbicides. The present sequence represents a PCR  
 CC primer used in an exemplification of the invention.

XX Sequence 23 BP; 5 A; 7 C; 5 G; 6 T; 0 other;

Query Match 65.0%; Score 13; DB 21; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 gctgctggtgaa 20  
 |||||

Db 20 GCTGCTGGTGAA 8

RESULT 13

AAC88395/c  
 ID AAC88395 standard; DNA; 23 BP.

XX AAC88395;

XX 02-MAR-2001 (first entry)

XX Primer Universal reverse.

XX Glyphosate; 5-enolpyruvylshikimate phosphate synthase; EPSPS;  
 XX herbicide resistance; ss.

XX Synthetic.

XX WO200066746-A1.

XX 09-NOV-2000.

XX 20-APR-2000; 2000WO-GB01559.

XX 29-APR-1999; 99GB-0009971.

XX 29-APR-1999; 99GB-0009972.

XX 29-JUL-1999; 99GB-0017837.

XX 29-JUL-1999; 99GB-0017842.

XX 21-DEC-1999; 99GB-0030190.

XX 21-DEC-1999; 99GB-0030206.

XX 21-DEC-1999; 99GB-0030214.

XX 21-DEC-1999; 99GB-0030216.

XX (ZENE ) ZENECA LTD.

XX Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;

XX WPI; 2000-679763/66.

XX Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate  
 XX synthase, used to produce glyphosate tolerant or resistant plants -  
 XX Example 20; Page 50; 85pp; English.

XX The present invention relates to a glyphosate resistant rice

XX 5-enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can

XX be used to produce plant tissue and/or morphologically normal fertile

XX whole plants which are tolerant or resistant to glyphosate herbicide,

XX and in the production of a herbicidal target for the high throughput

XX in vitro screening of potential herbicides.

Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 gctgctggtgaa 20  
 |||||

Db 20 GCTGCTGGTGAA 8

RESULT 14

AAC89319/c  
 ID AAC89319 standard; DNA; 23 BP.

XX AAC89319;

XX 07-MAR-2001 (first entry)

XX Primer universal reverse.

XX 5-enolpyruvylshikimate phosphate synthase; EPSPS;  
 XX herbicide resistance; glyphosate; ss.

XX Synthetic.

XX WO200066747-A1.

XX 09-NOV-2000.

XX 20-APR-2000; 2000WO-GB01572.

XX 29-APR-1999; 99GB-0009967.

XX 29-APR-1999; 99GB-0009969.

XX 29-APR-1999; 99GB-0009972.

XX 29-APR-1999; 99GB-0009981.

XX 29-APR-1999; 99GB-0017835.

XX 29-JUL-1999; 99GB-0017836.

XX 29-JUL-1999; 99GB-0017843.

XX 21-DEC-1999; 99GB-0030202.

XX 21-DEC-1999; 99GB-0030210.

XX 21-DEC-1999; 99GB-0030212.

XX (ZENE ) ZENECA LTD.

XX Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;

XX WPI; 2000-679764/66.

XX Isolated polynucleotide encoding a 5-enolpyruvylshikimate phosphate  
 XX synthase from rice is used for producing transgenic plants with  
 XX enhanced resistance to glyphosate herbicide -  
 XX Example 20; Page 49; 98pp; English.

XX The present invention relates to an Oryza sp. 5-enolpyruvylshikimate

XX phosphate synthase (EPSPS) gene. Vectors containing the gene may be

XX used to produce plant tissues and fertile whole plants which are

XX substantially tolerant or substantially resistant to glyphosate

XX herbicide and to produce a herbicidal target which is used for high

XX throughput in vitro screening of potential herbicides.

XX Sequence 23 BP; 5 A; 7 C; 5 G; 6 T; 0 other;

Query Match

Best Local Similarity 65.0%; Score 13; DB 21; Length 23;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 gctgctggtgaa 20

Db 20 GCTGCTGGTGAA 8

RESULT 15

AAA82953/c

ID AAA82953 standard; DNA; 19 BP.  
XX  
AC AAA82953;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE cdk6 ribozyme binding site #13.  
XX  
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;  
KW restenosis; ss.  
XX  
OS Mammalia.  
XX  
PN WO200032765-A2.  
XX  
PD 08-JUN-2000.  
XX  
PF 06-DEC-1999; 99WO-US28772.  
XX  
PR 04-DEC-1998; 98US-0110954.  
XX  
PA (IMMU-) IMMUSOL INC.  
XX  
PI Tritz R, Welch PJ, Barber JR, Robbins JM;  
XX  
DR WPI; 2000-412314/35.  
XX  
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
PT PCNA and Cyclin B1  
XX  
PS Disclosure; Page 54; 109pp; English.  
XX  
XX The present invention relates to a hairpin or hammerhead ribozyme,  
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
CC Representative examples of ribozyme recognition sites are given in  
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
CC inhibiting restenosis by introduction of the ribozyme into cells.  
CC The ribozyme is resistant to endonuclease activity and hence is  
CC efficient in restenosis treatment.  
XX  
SQ Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 19;  
Best Local Similarity 87.5%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 cctcgtcgtggtgga 19  
| | | | | | | | | |  
Db 17 CCTCGGGATGCTGGA 2

Search completed: October 2, 2001, 16:18:45  
Job time: 15489 sec

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:51 ; Search time 417.38 seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggaggagctcagtggtgg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-16
2	15	75.0	15	3	US-09-377-310-36
c 3	13.2	66.0	18	2	US-08-585-684B-2592
c 4	13.2	66.0	18	4	US-09-038-073-2592
5	13.2	66.0	20	3	US-09-166-186-87
6	13.2	66.0	20	4	US-09-313-932-87
c 7	13.2	66.0	47	1	US-08-171-389-275
c 8	13.2	66.0	47	1	US-08-123-936-275
c 9	13.2	66.0	47	2	US-08-475-228A-275
c 10	13.2	66.0	47	3	US-08-482-080A-275
c 11	13.2	66.0	47	5	PCT-US93-12388-275
c 12	12.8	64.0	30	1	US-08-049-283A-21
c 13	12.8	64.0	47	1	US-08-171-389-285
14	12.8	64.0	47	1	US-08-123-936-285
15	12.8	64.0	47	2	US-08-475-228A-285
16	12.8	64.0	47	3	US-08-482-080A-285
17	12.8	64.0	47	5	PCT-US93-12388-285
c 18	12.6	63.0	28	2	US-08-477-890-2
c 19	12.6	63.0	28	2	US-08-467-034A-2
c 20	12.6	63.0	28	4	US-08-468-646A-2
21	12.6	63.0	29	3	US-08-792-108A-3
c 22	12.6	63.0	31	3	US-08-929-140-14
c 23	12.6	63.0	32	1	US-08-246-123C-2
c 24	12.6	63.0	32	2	US-08-751-233A-2
c 25	12.6	63.0	33	1	US-07-834-539A-76
c 26	12.6	63.0	33	2	US-08-800-353-76
27	12.6	63.0	49	1	US-07-960-982-23

c 28	12.4	62.0	30	1	US-08-049-283A-22	Sequence 22, Appl
29	12.4	62.0	30	3	US-08-881-037-81	Sequence 81, Appl
c 30	12.2	61.0	26	1	US-07-796-106-16	Sequence 16, Appl
31	12	60.0	29	1	US-08-418-859-31	Sequence 31, Appl
32	12	60.0	29	1	US-08-418-859-32	Sequence 32, Appl
33	12	60.0	29	2	US-08-643-181-31	Sequence 31, Appl
34	12	60.0	29	2	US-08-643-181-32	Sequence 32, Appl
c 35	12	60.0	33	4	US-08-943-529-1	Sequence 1, Appl
36	12	60.0	38	2	US-08-839-581A-23	Sequence 23, Appl
37	12	60.0	38	4	US-05-023-591A-23	Sequence 23, Appl
38	12	60.0	40	1	US-08-050-132A-11	Sequence 11, Appl
39	12	60.0	40	3	US-08-815-652B-11	Sequence 11, Appl
c 40	11.8	59.0	19	1	US-08-602-036A-17	Sequence 17, Appl
c 41	11.8	59.0	19	2	US-08-502-374A-17	Sequence 17, Appl
c 42	11.8	59.0	19	2	US-08-642-407A-17	Sequence 17, Appl
c 43	11.8	59.0	22	3	US-08-928-881-12	Sequence 12, Appl
c 44	11.8	59.0	23	1	US-08-189-237-5	Sequence 5, Appl
45	11.8	59.0	26	1	US-07-834-539A-77	Sequence 77, Appl

#### ALIGNMENTS

RESULT 1  
US-09-377-310-16  
; Sequence 16, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-16

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaggaggagctcagtggtgg 20  
|||||

Db 1 ctaggaggagctcagtggtgg 20  
|||||

#### RESULT 2

US-09-377-310-36  
; Sequence 36, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-36

```

Query Match	75.0%;	Score 15;	DB 3;	Length 15;
Best Local Similarity	100.0%;	Pred. NO. 46;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels	

Oy 3 aggggaggtcagtq 17  
| | | | |  
Db 1 aggggaggtcagtq 15

RESULT 3  
US-08-585-684B-2592/c  
Sequence 2592, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McGSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.

Query Match 66.0%; Score 13.2; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels

Qy 1 ctaggggaggctcagtg 18  
|||  
Db 18 CTGGGGGAGGCTCAGCGT 1

## RESULT 4

US-09-038-073-2592/c  
 ; Sequence 2592, Application US/09038073  
 ; Patent No. 6194150  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Stinchcomb, Daniel T.  
 ; APPLICANT: Jarvis, Thale  
 ; APPLICANT: McSwiggen, James  
 ;  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 ; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 ;  
 ; NUMBER OF SEQUENCES: 2751  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Fastseq Version 1.5  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/038,073  
 ; FILING DATE:  
 ;  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/585,684  
 ; FILING DATE:  
 ;  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 218/078  
 ;  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ;  
 ; INFORMATION FOR SEQ ID NO: 2592:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ;  
 ; US-09-038-073-2592

Query Match 66.0%; Score 13.2; DB 4; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 15: Conservative 0; Mismatches 3; Indels

Qy	1	ctaggggaggtcagtg	18
Db	18	CTGGGGGAGGCTCAGGGT	1

RESULT 5  
US-09-166-87-87  
; Sequence 87, Application US/09166186A  
; Patent No. 6080580  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Brenda  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Butler, Madeline M.  
; APPLICANT: Shanahan, William R.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES  
; FILE REFERENCE: ISPH-0322  
; CURRENT APPLICATION NUMBER: US/09/166-87-87  
; CURRENT FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 250  
; SEQ ID NO 87  
; LENGTH: 20

```
; TYPE: DNA
-; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-166-186-87

Query Match      66.0%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 aggggaggtcagtggtg 20
   ||||| |||||
Db 1 agaggaggtcagtggtg 18

RESULT 6
US-09-313-932-87
; Sequence 87, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313.932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-313-932-87

Query Match      66.0%; Score 13.2; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 aggggaggtcagtggtg 20
   ||||| |||||
Db 1 agaggaggtcagtggtg 18

RESULT 7
US-08-171-389-275/c
; Sequence 275, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,936
; FILING DATE:

Query Match      66.0%; Score 13.2; DB 1; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tagggaggtcagtggtg 19
   ||||| |||||
Db 22 TAGGCAGGCTCTGTTG 5

RESULT 8
US-08-123-936-275/c
; Sequence 275, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,936
; FILING DATE:

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human estrogen-responsive gene pS2
US-08-171-389-275
```

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 275:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human estrogen-responsive gene ps2  
US-08-123-936-275

Query Match 66.0%; Score 13.2; DB 1; Length 47;  
Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tagggaggctcagtgtg 19  
||||| ||||| |||||

Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 9  
US-08-475-228A-275/c  
Sequence 275, Application US/08475228A  
Patent No. 5869241  
GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.  
APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
APPLICANT: Fry, Kirk E.  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
TITLE OF INVENTION: Molecules, Compositions and Methods  
NUMBER OF SEQUENCES: 664  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,228A  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,936  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/081,070  
FILING DATE: 22-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 275:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human estrogen-responsive gene ps2  
US-08-475-228A-275

Query Match 66.0%; Score 13.2; DB 2; Length 47;  
Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tagggaggctcagtgtg 19  
||||| ||||| |||||

Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 10  
US-08-482-080A-275/c  
Sequence 275, Application US/08482080A  
Patent No. 6010849  
GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.  
APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
APPLICANT: Fry, Kirk E.  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
TITLE OF INVENTION: Molecules, Compositions and Methods  
NUMBER OF SEQUENCES: 664  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,080A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/171,389  
FILING DATE: 20-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,936  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 275:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human estrogen-responsive gene p52
; US-08-482-080A-275

Query Match 66.0%; Score 13.2; DB 3; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtgtg 19
||||| ||||| |||||
Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 11
PCT-US93-12388-275/c
; Sequence 275, Application PC/TUS9312388
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12388
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 275:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human estrogen-responsive gene p52
; PCT-US93-12388-275

Query Match 66.0%; Score 13.2; DB 5; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtgtg 19
||||| ||||| |||||
Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 12
US-08-049-283A-21/c
; Sequence 21, Application US/08049283A
; Patent No. 5502176
; GENERAL INFORMATION:
; APPLICANT: Tenen, Daniel G.
; APPLICANT: Pahl, Heike L.
; APPLICANT: Burn, Timothy C.
; TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,283A
; FILING DATE: 14-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/020,465
; FILING DATE: 19-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/837,776
; FILING DATE: 13-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BIH91-03/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-049-283A-21

Query Match 64.0%; Score 12.8; DB 1; Length 30;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ggggaggctcagtgtg 19
```

RESULT 14

Sequence 285, Application US/08123936  
Patent No. 5726014  
GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.  
APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
TITLE OF INVENTION: Screening Assay for the Detection of  
DNA-Binding Molecules  
NUMBER OF SEQUENCES: 640  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,936  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 285:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human SAAL beta gene  
IS-08-123-936-285

Query Match	64.0%;	Score 12.8;	DB 1;	Length 47;
Best Local Similarity	97.8%;	Pred. No. 5.7e+02;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps 0;				
QY	3	aggggaggtcagtgt	18	
	8	AGGGAGGCTCAGTAT	23	

RESULT 15  
US-08-475-228A-285  
; Sequence 285, Application US/08475228A  
; Patent No. 5869241  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Cynthia A.  
; APPLICANT: Cantor, Charles R.  
; APPLICANT: Andrews, Beth M.  
; APPLICANT: Turin, Lisa M.



APPLICANT: Fry, Kirk E.  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
Molecules, Compositions and Methods  
NUMBER OF SEQUENCES: 664  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,228A  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,936  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/081,070  
FILING DATE: 22-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 285:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human SAAL beta gene  
US-08-475-228A-285

Query Match 64.08; Score 12.8; DB 2; Length 47;  
Best Local Similarity 87.5%; Pred. No. 5.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 agggaggagctcagtg 18  
|||||  
Db 8 AGGGAAGGCTCAGTAT 23

Search completed: October 2, 2001, 16:03:51  
Job time: 14595 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:43 ; Search time 876.95 Seconds  
(without alignments)  
14.320 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggaggagctcagtgtgg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0601:\*

1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT:\*

2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT:\*

3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT:\*

4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT:\*

5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT:\*

6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT:\*

7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT:\*

8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT:\*

9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT:\*

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15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT:\*

16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT:\*

17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT:\*

18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT:\*

19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT:\*

20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT:\*

21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT:\*

22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65548 Human focal adhesi
2	15	75.0	15	22	AAC65568 Human focal adhesi
3	13.4	67.0	34	17	AAT18223 HBEGF DNA antisens
4	13.4	67.0	35	17	AAT18225 HBEGF DNA antisens
5	13.2	66.0	18	17	Human B7-2 hairpin
6	13.2	66.0	20	21	Human TNFalpha ant
7	13.2	66.0	21	22	Human clone p12616
8	13.2	66.0	33	18	AAT91995 Primer for human c
9	13.2	66.0	47	15	AAC069525 Human estrogen-res
10	13.2	66.0	47	18	AAT63967 Human oestrogen-re
11	13.2	66.0	47	20	AAX17275 Test sequence from

12	12.8	64.0	21	22	AAF96616 Human gene single
13	12.8	64.0	25	21	AAC66790 Human hyperpolaris
14	12.8	64.0	30	17	AAT14576 CDT1b gene promote
15	12.8	64.0	43	16	AA04232 pNIV3606 amplifica
16	12.8	64.0	47	15	AA069535 Human SAA1 beta ge
17	12.8	64.0	47	18	AAT63997 Human SAA1 beta ge
18	12.8	64.0	47	20	AAX17285 Test sequence from
19	12.6	63.0	27	17	AAT35053 HSV thymidine kina
20	12.6	63.0	28	19	AAV19540 Recombinant retrov
21	12.6	63.0	29	21	AAAL0258 Fibrinogen B-beta
22	12.6	63.0	31	20	AAAX3879 PCR primer for bet
23	12.6	63.0	32	18	AAT58070 Potyvirus P1 prote
24	12.6	63.0	32	20	AAZ23620 Reporter gene cons
25	12.6	63.0	32	21	AAC66808 Oligo "g" used in
26	12.6	63.0	33	20	AAAX0606 Hygromycin phospho
27	12.6	63.0	35	18	AAAX5277 Hygromycin phospho
28	12.6	63.0	35	20	AAAX58529 Hygromycin phospho
29	12.4	62.0	25	19	AAV39103 Primer CYP2DEIR us
30	12.4	62.0	30	13	AAQ25680 Sequence of 5' LH p
31	12.4	62.0	30	17	AAT14577 CDT1b gene promote
32	12.4	62.0	42	21	AAAS8778 PCR primer for Fv
33	12.4	62.0	42	21	AAAS8779 PCR primer for Fv
34	12.2	61.0	20	22	AAC60289 Primer R2 used to
35	12.2	61.0	25	21	AAC66789 Human hyperpolaris
36	12.2	61.0	26	14	AAQ34833 PCR primer #1 to a
37	12.2	61.0	30	19	AAV11129 SH2 binding protei
38	12.2	61.0	34	20	AAV7216 Constitutatory pro
39	12.2	61.0	34	21	AA250600 3' B7-2 primer to
40	12	60.0	16	22	AAZ27764 Human HIV-1 monocl
41	12	60.0	21	20	AAZ29888 Primer OS295 for m
42	12	60.0	25	21	AAZ51454 Human NK2R promote
43	12	60.0	29	14	AAQ37256 Minisatellite MS32
44	12	60.0	29	14	AAQ37257 Minisatellite MS32
45	12	60.0	29	17	AAT40160 MS32 minisatellite

ALIGNMENTS

RESULT 1

AAC65548

ID AAC65548 standard; DNA; 20 BP.

XX AC

XX AAC65548;

DT 12-FEB-2001 (first entry)

XX

DE Human focal adheslon kinase antisense sequence #14.

XX

KW Human; focal adheslon kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX

OS Homo sapiens.

XX

PN US6133031-A.

XX

PD 17-OCT-2000.

XX

PF 19-AUG-1999; 99US-0377310.

XX

PR 19-AUG-1999; 99US-0377310.

XX

(ISIS-) ISIS PHARM INC.

PI Monia BP, Gaarde WA;

XX

DR WPI; 2001-006141/01.

XX

PT New antisense compounds for inhibiting focal adheslon kinase

PT expression, especially useful for inhibiting retinal

XX neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Claim 3: Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
 CC is involved in integrin-mediated signal transduction, and is implicated  
 CC in cancer, particularly colon, breast and oral tumours, embryonic  
 CC development disorders, angiogenic disorders and wound healing. The  
 CC antisense sequences, including the one shown here, can be used in the  
 CC treatment of all of these.

XX Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaggggaggctcagtggtg 20  
 |||||

Db 1 ctaggggaggctcagtggtg 20  
 |||||

#### RESULT 2

AAC65568  
 ID AAC65568 standard; DNA; 15 BP.

XX AAC65568;

XX 12-FEB-2001 (first entry)

DE Human focal adhesion kinase antisense sequence #34.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;  
 KW embryonic development disorder; angiogenic disorder; wound healing;  
 KW antisense; phosphorothioate; ss.

XX Homo sapiens.

XX US6133031-A.

XX 17-OCT-2000.

XX 19-AUG-1999; 990S-0377310.

XX 19-AUG-1999; 990S-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Montla BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase  
 PT expression, especially useful for inhibiting retinal  
 PT neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Example 2; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
 CC is involved in integrin-mediated signal transduction, and is implicated  
 CC in cancer, particularly colon, breast and oral tumours, embryonic  
 CC development disorders, angiogenic disorders and wound healing. The  
 CC antisense sequences, including the one shown here, can be used in the  
 CC treatment of all of these.

XX Sequence 15 BP; 3 A; 2 C; 8 G; 2 T; 0 other;

Query Match 75.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 aggggaggctcagtg 17  
 |||||

Db 1 aggggaggctcagtg 15  
 |||||

#### RESULT 3

AAT18223  
 ID AAT18223 standard; DNA; 34 BP.

XX AAT18223;

XX 24-JUN-1996 (first entry)

XX HBEGF DNA antisense primer.

XX HBEGF; heparin-binding epidermal-like growth factor; saporin;  
 KW cytotoxic; ribosome-inactivating protein; targeted delivery; tumour;  
 KW breast cancer; bladder cancer; restenosis; therapy; primer; PCR;  
 KW polymerase chain reaction; ss.

XX Synthetic.

XX WO9608274-A2.

XX 21-MAR-1996.

XX 13-SEP-1995; 95WO-US12205.

XX 16-MAY-1995; 95US-0441979.

XX 13-SEP-1994; 94US-0305771.

XX (PRIZ-) PRIZM PHARM INC.

XX Chandler LA, Houston LL, McDonald JR, Nova MP, Sosnowski BA;

XX WPI; 1996-179728/18.

XX Conjugate comprising HBEGF polypeptide and targeted agent - used to  
 PT treat HBEGF-mediated pathophysiological conditions, e.g. solid  
 PT tumour and skin disorders

XX Example 6; Page 94; 163pp; English.

XX Sense and antisense PCR primers (AAT18222-23) were used to amplify  
 CC DNA (see AAT17958) coding for human heparin-binding epidermal-like  
 CC growth factor (HBEGF) (AAR92897) using p232B1 as template. The  
 CC PCR product has a 5' NcoI site and a 3' stop codon followed by  
 CC an SalI site. It was ligated into pET3AP-MCS (see AAT18220-21).  
 CC The resulting plasmid (p236B1) (see AAT18232) codes for a fusion  
 CC (AAR92921) of HBEGF and saporin linked by an Ala-Met-Ala linker.  
 CC This was expressed in Escherichia coli and is useful for targeting  
 CC cytotoxic saporin e.g. to solid tumour cells bearing the HBEGF  
 CC receptor.

XX Sequence 34 BP; 9 A; 8 C; 9 G; 8 T; 0 other;

Query Match 67.0%; Score 13.4; DB 17; Length 34;  
 Best Local Similarity 93.3%; Pred. No. 9e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ctaggggaggctcag 15  
 |||||

Db 11 ctatgggaggctcag 25

#### RESULT 4

AAT18225  
 ID AAT18225 standard; DNA; 35 BP.

XX AAT18225;

XX 24-JUN-1996 (first entry)

XX DE HBEGF DNA antisense primer.  
 XX KW HBEGF: heparin-binding epidermal-like growth factor; saporin;  
 KW cytotoxic; ribosome-inactivating protein; targeted delivery; tumour;  
 KW breast cancer; bladder cancer; restenosis; therapy; primer; PCR;  
 KW polymerase chain reaction; baculovirus; ss.  
 XX OS Synthetic.  
 XX PN WO9608274-A2.  
 XX PD 21-MAR-1996.  
 XX PF 13-SEP-1995; 95WO-US12205.  
 XX PR 16-MAY-1995; 95US-0441979.  
 XX PR 13-SEP-1994; 94US-0305771.  
 XX PA (PRIZ-) PRIZM PHARM INC.  
 XX PI Chandler LA, Houston LL, McDonald JR, Nova MP, Sosnowski BA;  
 XX WPI; 1996-179728/18.  
 XX DR Conjugate comprising HBEGF polypeptide and targeted agent - used to  
 XX treat HBEGF-mediated patho:physiological conditions, e.g. solid  
 XX tumour and skin disorders  
 XX PS Example 8; Page 96; 163pp; English.  
 XX CC An antisense PCR primer (AAT18225) was used with sense primers  
 CC (AAT18224 or AAT18227) to amplify DNA (see AAT17958) coding for  
 CC human heparin-binding epidermal-like growth factor (HBEGF)  
 CC (AAR92897) using p3281 as template. The PCR products were  
 CC ligated into pBlueac111 (invitrogen) (see AAT18226 and AAT18228)  
 CC and used for baculovirus expression of HBEGF. Conjugates of  
 CC HBEGF with saporin are useful for targeted treatment of e.g.  
 XX solid tumours.  
 XX SQ Sequence 35 BP; 10 A; 8 C; 8 G; 9 T; 0 other;  
 Query Match 67.0%; Score 13.4; DB 17; Length 35;  
 Best Local Similarity 93.3%; Pred. No. 9e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 ctatggggaggctcag 15  
 ||| |||||  
 Db 12 ctatggggaggctcag 26  
 RESULT 5  
 AAX67092/c  
 ID AAX67092 standard; RNA; 18 BP.  
 XX AC AAX67092;  
 XX DT 20-JUL-1999 (first entry)  
 XX DE Human B7-2 hairpin ribozyme target SEQ ID NO:3724.  
 XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
 KW diagnosis; ss.  
 XX OS Homo sapiens.  
 XX PN WO9618736-A2.  
 XX PD 20-JUN-1996.

XX PF 22-NOV-1995; 95WO-US15516.  
 XX PR 05-OCT-1995; 95US-0541365.  
 PR 13-DEC-1994; 94US-0354920.  
 PR 23-DEC-1994; 94US-0363253.  
 PR 23-DEC-1994; 94US-0363254.  
 PR 17-FEB-1995; 95US-0390850.  
 PR 20-APR-1995; 95US-0426124.  
 PR 02-MAY-1995; 95US-0432874.  
 PR 04-MAY-1995; 95US-0434509.  
 PR 07-JUL-1995; 95US-0000951.  
 PR 07-JUL-1995; 95US-0000974.  
 PR 07-AUG-1995; 95US-0512861.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PI Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;  
 PI Beigelman L, Karpeisky A, Modak A, Usman N, Burgin A;  
 PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;  
 XX DR WPI; 1996-300653/30.  
 XX EN Enzymatic nucleic acid molecules having a hammer-head motif - used  
 XX for the treatment of arthritis, induction of graft tolerance or  
 XX treatment of auto-immune diseases  
 XX PS Claim 10; Page 216; 307pp; English.  
 XX CC The present invention describes a novel enzymatic nucleic acid (ENA)  
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose  
 CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)  
 CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.  
 CC The ENA's can inhibit collagenase and stromelysin production in the  
 CC synovial membrane of joints for the treatment or prevention of arthritis,  
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
 CC be used to treat antigen presenting cells of a donor to induce tolerance  
 CC in a recipient to an alloantigen of a donor. They can also be used for  
 CC enhancing graft tolerance or for treating autoimmune disease, and for  
 CC treating allergies and other inflammatory conditions. The ENA's can also  
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
 CC stromelysin without introducing the non-specific effects upon gene  
 CC expression which accompany treatment with retinoids and dexamethasone.  
 CC The concentration of ribozyme required to affect a therapeutic treatment  
 CC is lower than that required of antisense molecules, and is highly  
 CC specific. The present sequence is used in the exemplification of the  
 CC present invention.  
 XX SQ Sequence 18 BP; 3 A; 11 C; 2 G; 2 U; 0 other;  
 Query Match 66.0%; Score 13.2; DB 17; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ctatggggaggctcagtg 18  
 || |||||  
 Db 18 CTGGGGGAGGCTGAGGT 1  
 RESULT 6  
 AAA40846  
 ID AAA40846 standard; DNA; 20 BP.  
 XX AC AAA40846;  
 XX DT 16-AUG-2000 (first entry)  
 XX DE Human TNFalpha antisense oligonucleotide ISIS# 21706.  
 XX KW Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;  
 KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;  
 KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;

KW pancreatitis; atopic dermatitis; allograft rejection;  
 XX autoimmune disease; inflammatory disease; ss.  
 OS Synthetic.

XX

PN WO200020645-A1.

XX 13-APR-2000.

PD

XX 05-OCT-1999; 99WO-US23205.

XX 05-OCT-1998; 98US-0166186.

PR 18-MAY-1999; 99US-0313932.

XX (ISIS-) ISIS PHARM INC.

XX Baker BF, Bennett CF, Butler MM, Shanahan WJ;

XX WPI; 2000-303808/26.

XX Oligonucleotide for treating diseases associated with human tumour

XX necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid

XX arthritis, comprises nucleotide sequence complementary to intron of

XX nucleic acid encoding TNFalpha -

XX Example 6; Page 58; 283pp; English.

XX This sequence represents an antisense oligonucleotide sequence which

XX targets a region of the human tumour necrosis factor alpha (TNFalpha)

XX nucleotide sequence. TNFalpha is an important cytokine that plays a role

XX in host defence. It is produced mainly in macrophages and monocytes in

XX response to infection, invasion, injury or inflammation. Overexpression

XX of TNFalpha can result in disease states, particularly in infectious,

XX inflammatory and autoimmune diseases. The invention relates to antisense

XX oligonucleotides, such as that represented by the present sequence which

XX are capable of modulating the TNFalpha gene expression. The

XX oligonucleotides optionally have a phosphorothioate backbone, and may

XX also optionally contain at least one 2'-O-methoxyethyl modification. The

XX oligonucleotides are useful for modulating the expression of human

XX TNFalpha in cells and tissues, reducing a human cell inflammatory

XX response, reducing the blood glucose level in a human and treating a

XX human having a disease or condition associated with TNFalpha. Examples of

XX diseases associated with TNFalpha include diabetes, inflammatory bowel

XX disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,

XX infectious disease, hepatitis, atopic dermatitis or allograft rejection.

XX The antisense oligonucleotides are also useful for modulating the

XX function of a selected nucleic acid sequence in adipose tissue.

XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;

XX

KW pancreatitis; atopic dermatitis; allograft rejection;  
 XX autoimmune disease; inflammatory disease; ss.  
 OS Synthetic.

XX

PN WO200020645-A1.

XX 13-APR-2000.

PD

XX 05-OCT-1999; 99WO-US23205.

XX 05-OCT-1998; 98US-0166186.

PR 18-MAY-1999; 99US-0313932.

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XX disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,

XX infectious disease, hepatitis, atopic dermatitis or allograft rejection.

XX The antisense oligonucleotides are also useful for modulating the

XX function of a selected nucleic acid sequence in adipose tissue.

XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;

XX

KW chromosome 2q11; ss.

XX Homo sapiens.

XX WO200073320-A1.

XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US14572.

XX 27-MAY-1999; 99US-0322134.

XX (HYSE-) HYSEQ INC.

XX Ford J, Yeung G;

XX WPI; 2001-041140/05.

XX New chemokine polypeptide from fetal liver-spleen, useful in gene

XX therapy, especially for modulating hematopoiesis, or immune or

XX inflammatory responses, e.g. for repairing tissues or treating

XX autoimmune disorders -

XX Example 3; Page 78; 92pp; English.

XX The present sequence is a PCR primer for human clone AAP12616HY coding

XX sequence (see AAC90427). The AAP12616HY coding sequence is useful for

XX modulating the immune and inflammatory responses, and hematopoiesis; and

XX in gene therapy for treating allergies (e.g. asthma), autoimmune

XX disorders (e.g. arthritis or transplantation rejection), in tissue

XX repair and replacement, or wound healing (e.g. treatment of burns,

XX treatment of surgical incisions and ulcers, such as stomach or diabetic

XX ulcers). The AAP12616HY coding sequence is thought to encode a chemokine

XX and is located on chromosome 2q11.

XX Sequence 21 BP; 7 A; 7 C; 4 G; 3 T; 0 other;

XX

XX Query Match 66.0%; Score 13.2; DB 22; Length 21;

XX Best Local Similarity 83.3%; Pred. No. 1.1e+03;

XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX QY 3 agggaggagtcagtggtgg 20

XX || || || || || || || || ||

XX Db 19 AGTGCAGTCTCAGTGTGG 2

XX

XX RESULT 8

XX AAT91995/c

XX ID AAT91995 standard; DNA; 33 BP.

XX

XX AAT91995;

XX

XX 08-APR-1998 (first entry)

XX

XX Primer for human chemokine alpha-3 cDNA.

KW pancreatitis; atopic dermatitis; allograft rejection;  
 XX autoimmune disease; inflammatory disease; ss.  
 OS Synthetic.

XX

PN WO200020645-A1.

XX 13-APR-2000.

PD

XX 05-OCT-1999; 99WO-US23205.

XX 05-OCT-1998; 98US-0166186.

PR 18-MAY-1999; 99US-0313932.

XX (ISIS-) ISIS PHARM INC.

XX Baker BF, Bennett CF, Butler MM, Shanahan WJ;

XX WPI; 2000-303808/26.

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XX necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid

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XX response to infection, invasion, injury or inflammation. Overexpression

XX of TNFalpha can result in disease states, particularly in infectious,

XX inflammatory and autoimmune diseases. The invention relates to antisense

XX oligonucleotides, such as that represented by the present sequence which

XX are capable of modulating the TNFalpha gene expression. The

XX oligonucleotides optionally have a phosphorothioate backbone, and may

XX also optionally contain at least one 2'-O-methoxyethyl modification. The

XX oligonucleotides are useful for modulating the expression of human

XX TNFalpha in cells and tissues, reducing a human cell inflammatory

XX response, reducing the blood glucose level in a human and treating a

XX human having a disease or condition associated with TNFalpha. Examples of

XX diseases associated with TNFalpha include diabetes, inflammatory bowel

XX disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,

XX infectious disease, hepatitis, atopic dermatitis or allograft rejection.

XX The antisense oligonucleotides are also useful for modulating the

XX function of a selected nucleic acid sequence in adipose tissue.

XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;

XX

KW pancreatitis; atopic dermatitis; allograft rejection;  
 XX autoimmune disease; inflammatory disease; ss.  
 OS Synthetic.

XX

PN WO200020645-A1.

XX 13-APR-2000.

PD

XX 05-OCT-1999; 99WO-US23205.

XX 05-OCT-1998; 98US-0166186.

PR 18-MAY-1999; 99US-0313932.

XX (ISIS-) ISIS PHARM INC.

XX Baker BF, Bennett CF, Butler MM, Shanahan WJ;

XX WPI; 2000-303808/26.

XX Oligonucleotide for treating diseases associated with human tumour

XX necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid

XX arthritis, comprises nucleotide sequence complementary to intron of

XX nucleic acid encoding TNFalpha -

XX Example 6; Page 58; 283pp; English.

XX This sequence represents an antisense oligonucleotide sequence which

XX targets a region of the human tumour necrosis factor alpha (TNFalpha)

XX nucleotide sequence. TNFalpha is an important cytokine that plays a role

XX in host defence. It is produced mainly in macrophages and monocytes in

XX response to infection, invasion, injury or inflammation. Overexpression

XX of TNFalpha can result in disease states, particularly in infectious,

XX inflammatory and autoimmune diseases. The invention relates to antisense

XX oligonucleotides, such as that represented by the present sequence which

XX are capable of modulating the TNFalpha gene expression. The

XX oligonucleotides optionally have a phosphorothioate backbone, and may

XX also optionally contain at least one 2'-O-methoxyethyl modification. The

XX oligonucleotides are useful for modulating the expression of human

XX TNFalpha in cells and tissues, reducing a human cell inflammatory

XX response, reducing the blood glucose level in a human and treating a

XX human having a disease or condition associated with TNFalpha. Examples of

XX diseases associated with TNFalpha include diabetes, inflammatory bowel

XX disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,

XX infectious disease, hepatitis, atopic dermatitis or allograft rejection.

XX The antisense oligonucleotides are also useful for modulating the

XX function of a selected nucleic acid sequence in adipose tissue.

XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;

XX

KW pancreatitis; atopic dermatitis; allograft rejection;  
 XX autoimmune disease; inflammatory disease; ss.  
 OS Synthetic.

XX

PN WO200020645-A1.

XX 13-APR-2000.

PD

XX 05-OCT-1999; 99WO-US23205.

XX 05-OCT-1998; 98US-0166186.

PR 18-MAY-1999; 99US-0313932.

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XX response to infection, invasion, injury or inflammation. Overexpression

XX of TNFalpha can result in disease states, particularly in infectious,

XX inflammatory and autoimmune diseases. The invention relates to antisense

XX oligonucleotides, such as that represented by the present sequence which

XX are capable of modulating the TNFalpha gene expression. The

XX oligonucleotides optionally have a phosphorothioate backbone, and may

XX also optionally contain at least one 2'-O-methoxyethyl modification. The

XX oligonucleotides are useful for modulating the expression of human

XX TNFalpha in cells and tissues, reducing a human cell inflammatory

XX response, reducing the blood glucose level in a human and treating a

XX human having a disease or condition associated with TNFalpha. Examples of

XX diseases associated with TNFalpha include diabetes, inflammatory bowel

XX disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,

XX infectious disease, hepatitis, atopic dermatitis or allograft rejection.

XX The antisense oligonucleotides are also useful for modulating the

XX function of a selected nucleic acid sequence in adipose tissue.

XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;

XX

KW pancreatitis; atopic dermatitis; allograft rejection;  
 XX autoimmune disease; inflammatory disease; ss.  
 OS Synthetic.

XX

PN WO200020645-A1.

XX 13-APR-2000.

PD

XX 05-OCT-1999; 99WO-US23205.

XX 05-OCT-1998; 98US-

PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Li H, Ni J, Su JY;  
 XX WPI; 1997-480232/44.  
 XX Polynucleotide(s) encoding human chemokine alpha-3 - used to treat  
 PT tumours, chronic infections, autoimmune diseases, parasitic  
 PT infections, psoriasis, asthma etc.  
 XX Example 3; Page 54; 69pp; English.  
 XX The present sequence is a primer for the cDNA encoding human  
 CC chemokine alpha-3 (CK alpha-3). CK alpha-3 can be used to treat  
 CC tumours, chronic infections, leukaemia, T-cell mediated autoimmune  
 CC diseases, parasitic infections, psoriasis, asthma and allergy. It  
 CC can also be used to regulate haematopoiesis, stimulate growth  
 CC factor activity, inhibit angiogenesis and promote wound healing.  
 XX Sequence 33 BP; 8 A; 14 C; 7 G; 4 T; 0 other;  
 SQ

Query Match 66.08; Score 13.2; DB 18; Length 33;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 agggaggctcagtggtg 20  
 | | | | | | | | | |  
 Db 28 ACGGAGGCTCATGTGG 11

RESULT 9  
 ID AAQ69525/C  
 AC AAQ69525 standard; DNA; 47 BP.  
 XX  
 XX  
 XX  
 DT 01-MAR-1995 (first entry)  
 DE Human estrogen-responsive gene pS2 target region.  
 XX  
 KW DNA protein-binding assay; test sequence; screening sequence;  
 KW promoter; target; TATA box; Herpes Simplex Virus; HSV;  
 KW origin of replication; UL9; transcription factor; TFIIID: ds.  
 XX Synthetic.  
 OS  
 PN W09414980-A.  
 XX  
 XX  
 PD 07-JUL-1994.  
 XX  
 PF 20-DEC-1993; 93WO-US12388.  
 XX  
 PR 23-DEC-1992; 92US-0996783.  
 PR 17-SEP-1993; 93US-0123936.  
 XX  
 PA (GENE-) GENELABS TECHNOLOGIES INC.  
 XX  
 PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;  
 XX  
 XX WPI; 1994-234711/28.  
 XX  
 PT Sequence-directed DNA-binding molecules - useful in  
 PT pharmaceuticals and as molecular reagents  
 XX  
 XX Claim 28; Page 349; 587pp; English.  
 XX  
 CC A DNA protein-binding assay is provided, useful for screening  
 CC libraries of synthetic or biological cnds. for their ability  
 CC to bind DNA test sequences. The assay is versatile in that any  
 CC number of test sequences can be tested by placing the test sequence  
 CC adjacent to a defined protein-binding screening sequence. Binding  
 CC of mols. to these test sequences changes the binding characteristics

CC of the protein mol. to its cognate binding sequence. When such a mol.  
 CC binds the test sequence, the equilibrium of the DNA:protein complexes  
 CC is disturbed, generating changes in the concentration of free DNA probe.  
 CC One application of this method is to eucaryotic general transcription  
 CC factors (e.g. TFIIID), where the target region is typically selected  
 CC from DNA sequences adjacent to the binding site for the eucaryotic  
 CC transcription factor. Numerous exemplary test sequences are given:  
 CC the sequences in AAQ69251-731 and AAQ69850 correspond to promoter  
 CC targets (typically, TATA box-contg. sites) for human genes and the  
 CC sequences in AAQ69732-849 correspond to promoter targets for viral genes.  
 CC The test sequences may also be randomly generated. DNA:protein  
 CC interaction may be used for screening purposes, e.g. the Herpes Simplex  
 CC Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and  
 CC AAQ69891).  
 XX  
 SQ Sequence 47 BP; 12 A; 15 C; 13 G; 7 T; 0 other;  
 Query Match 66.08; Score 13.2; DB 15; Length 47;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtggtg 19  
 | | | | | | | | | |  
 Db 22 TAGGCGAGGCTCTGTGG 5

RESULT 10  
 ID AAT63987/C  
 AC AAT63987 standard; DNA; 47 BP.  
 XX  
 XX AAT63987;  
 XX  
 DT 17-MAR-1997 (first entry)  
 DE Human oestrogen-responsive gene, pS2, TFIIID binding site.  
 XX  
 KW Duplex DNA; target region; binding characteristic; DNA binding protein;  
 KW TFIIID; transcription factor; binding site; inhibition; enhance;  
 KW inherited genetic disorder; cancer; ds.  
 XX Homo sapiens.  
 OS  
 PN US5578444-A.  
 XX  
 XX 26-NOV-1996.  
 PD  
 PF 27-JUN-1991; 91US-0723618.  
 XX  
 PR 20-DEC-1993; 93US-0171389.  
 PR 27-JUN-1991; 91US-0723618.  
 PR 23-DEC-1992; 92US-0996783.  
 PR 17-SEP-1993; 93US-0123936.  
 XX  
 PA (GENE-) GENELABS TECHNOLOGIES INC.  
 XX  
 PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;  
 XX  
 XX WPI; 1997-020402/02.  
 XX  
 PT Altering binding characteristics of DNA binding proteins to duplex  
 PT DNA - by attaching specific small cpd. to target region close to the  
 PT protein's binding site, useful in treatment of viral disease, cancer  
 PT etc  
 XX  
 XX Claim 6; Column 239-240; 264pp; English.  
 XX  
 CC The sequences given in AAT63713-4312 represent duplex DNA's which act  
 CC as target regions in the method of the invention. The method for  
 CC altering the binding characteristics of a DNA-binding protein to duplex  
 CC DNA comprises contacting the duplex DNA with a small molecule which  
 CC binds sequence-specifically to a target region, where, when the small  
 CC molecule is bound to the target region, it is adjacent to, but not

CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.  
 CC The small molecule is added at a concentration effective to alter the  
 CC binding of the DNA binding protein, pref. TFID, to its binding site on  
 CC the duplex DNA. The binding of the small molecule may inhibit or  
 CC enhance the binding of the DNA-binding protein to its binding site. The  
 CC compounds isolated using this method are potentially useful as  
 CC therapeutic agents for treatment of any disease which involves a  
 CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.  
 CC The method is suitable for screening large biological or chemical  
 CC libraries and allows determination of sequence-specific and relative  
 CC affinities of known DNA-binding agents for different DNA sequences.  
 CC The design of these duplex DNA's allows a single DNA:protein interaction  
 CC to be used for screening sequence-specific, or preferential, DNA binding  
 CC proteins that recognise almost any possible sequence (see also AAT49539-  
 CC 74).

XX  
 SQ Sequence 47 BP; 12 A; 15 C; 13 G; 7 T; 0 other;

Query Match 66.0%; Score 13.2; DB 18; Length 47;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 taggggaggtcagtg 19  
 ||||| ||||| || ||  
 Db 22 TAGGGCAGGCTCTGTTTG 5

RESULT 11  
 AAX17275/C  
 ID AAX17275 standard; DNA; 47 BP.  
 XX  
 AC AAX17275;  
 XX  
 DT 06-MAY-1999 (first entry)  
 XX  
 DE Test sequence from human estrogenresponsive gene p52.

XX Test sequence; DNA-binding molecule; screening sequence; human;  
 KW nucleic acid amplification; target; viral; ds.  
 XX

OS Homo sapiens.

XX US5869241-A.

XX 09-FEB-1999.

XX 07-JUN-1995; 95US-0475228.

XX 20-DEC-1993; 93US-0171389.

PR 27-JUN-1991; 91US-0723618.

PR 23-DEC-1992; 92US-0996783.

PR 17-SEP-1993; 93US-0123936.

XX 07-JUN-1995; 95US-0475228.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

XX WPI; 1999-152755/13.

XX Determination of DNA sequence preference of a DNA-binding molecule -

XX based on inhibition of binding of protein to oligonucleotide

XX sequence attached to test sequence

XX Claim 3; Columns 241-242; 270pp; English.

XX Sequences AAX17001 to AAX17600 represent specifically claimed target  
 CC test sequences that are used in the method of the invention of  
 CC determining the DNA sequence preference of a DNA-binding molecule. The  
 CC method comprises: (i) adding a test molecule and a DNA-binding protein to  
 CC a mixture of duplex DNA test oligonucleotides, each of the test  
 CC oligonucleotides having a test sequence adjacent to a screening sequence,

CC where the screening sequence binds to the DNA-binding protein with a  
 CC binding affinity that is independent of the DNA sequence of the test  
 CC sequence, and where the mixture of duplex DNA test oligonucleotides  
 CC includes several test sequences; (ii) incubating the test molecule, the  
 CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein  
 CC for a time sufficient to permit binding of the test molecule to test  
 CC sequences in the duplex DNA; (iii) separating unbound test  
 CC oligonucleotides from test oligonucleotides bound to binding protein;  
 CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps  
 CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and  
 CC (vii) sequencing the isolated test oligonucleotides. Test sequences  
 CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human  
 CC genes and test sequences AAX17482-X17599 correspond to promoter targets  
 CC for viral genes.

XX  
 SQ Sequence 47 BP; 12 A; 15 C; 13 G; 7 T; 0 other;

Query Match 66.0%; Score 13.2; DB 20; Length 47;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 taggggaggtcagtg 19  
 ||||| ||||| || ||  
 Db 22 TAGGGCAGGCTCTGTTTG 5

RESULT 12

AAF96616

ID AAF96616 standard; DNA; 21 BP.

XX

AC AAF96616;

XX 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #1377.

DE Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

KW polymorphism; vascular disease; coronary artery disease; forensics;

KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

KW pulmonary embolism; paternity test; ds.

XX Homo sapiens.

XX OS

FH Key Location/Qualifiers

FT Variation replace(11,C)

FT /\*tag= a

FT /standard\_name= "single nucleotide polymorphism"

XX WO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000WO-US24503.

XX 10-SEP-1999; 99US-0153357.

PR 26-JUL-2000; 2000US-0220947.

PR 16-AUG-2000; 2000US-0225724.

XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;

XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in

XX applications such as forensics, paternity testing, medicine, genetic

XX analysis and phenotype correlations to diseases such as diabetes and

XX atherosclerosis -

XX Examples; Page 142; 242pp; English.



CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification.

XX Sequence 21 BP; 5 A; 2 C; 12 G; 2 T; 0 other;  
 SQ

Query Match 64.0%; Score 12.8; DB 22; Length 21;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 gggaggtcagtggtg 20  
 ||||| |||||  
 Db 6 gggaggtcagtggtg 21

RESULT 13  
 AAC66790/c  
 ID AAC66790 standard; cDNA: 25 BP.  
 XX  
 AC AAC66790;  
 XX  
 DT 16-FEB-2001 (first entry)  
 XX  
 DE Human hyperpolarisation-activated channel HAC3 PCR primer #11.  
 XX  
 KW Human; hyperpolarisation-activated channel; HAC3; neuroleptic; nootropic;  
 KW cerebrotective; antimigraine; antiarrhythmic; gene therapy;  
 KW pacemaker dysfunction; familial sinus rhythm disease;  
 KW sick sinus syndrome associated with atrial fibrillation;  
 KW sinus tachycardia; bradycardia; ventricular arrhythmia; bipolar disease;  
 KW schizophrenia; central nervous system disorder; migraine; seizure;  
 KW stroke; PCR primer; ss.

XX Homo sapiens.  
 OS  
 XX WO200063349-A1.  
 XX  
 PN 26-OCT-2000.  
 PD  
 XX 13-APR-2000; 2000WO-US09865.  
 PF  
 XX 15-APR-1999; 99US-0129456.  
 PR  
 XX (ICAG-) ICAGEN INC.  
 PA  
 XX Jegla TJ;  
 PI  
 XX WPI; 2000-679592/66.  
 DR  
 XX Novel human hyperpolarization activated channel 3 polypeptide useful to  
 PT identify hyperpolarization-activated cation channels modulators for  
 PT treating familial sinus rhythm diseases, and ventricular arrhythmias -  
 XX Example; Page 63; 81pp; English.

XX The present invention relates to the coding sequence and polypeptide  
 CC sequence for human hyperpolarisation activated channel 3 (HAC3) (see  
 CC AAC66779 and AAB28375). HAC3 comprises an alpha-subunit of a cation  
 CC channel, which forms upon hyperpolarisation, a cation channel with an  
 CC additional HAC. Modulators of HAC activity are useful for treating  
 CC various pacemaker dysfunctions such as familial sinus rhythm diseases,  
 CC sick sinus syndrome associated with atrial fibrillation, sinus  
 CC tachycardias and bradycardias as well as ventricular arrhythmias. The  
 CC modulators are also useful for treating other disorders involving

CC abnormal ion flux, e.g., memory and learning disorders, sleeping  
 CC disorders, bipolar disease, schizophrenia, central nervous system (CNS)  
 CC disorders such as migraines, hearing and vision problems, seizures, and  
 CC as neuroprotective agents (e.g. to prevent stroke). The Human HAC3 coding  
 CC sequence is useful for treating the disorders by gene therapy. The  
 CC present sequence is a PCR primer which can be used to isolate the human  
 CC HAC3 coding sequence.

XX Sequence 25 BP; 4 A; 15 C; 2 G; 4 T; 0 other;  
 SQ

Query Match 64.0%; Score 12.8; DB 21; Length 25;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 gggaggtcagtggtg 20  
 ||||| |||||  
 Db 18 GGGAGGCTGAGAGTGG 3

RESULT 14  
 AAT14576/c  
 ID AAT14576 standard; DNA: 30 BP.  
 XX  
 AC AAT14576;  
 XX  
 DT 24-SEP-1996 (first entry)  
 XX  
 DE CD11b gene promoter nucleotides -78 to -49 (wt-78).  
 XX  
 KW promoter; myeloid-specific; CD11b; Spl; PU.1; transcription factor;  
 KW binding; transcription start site; ss.

XX Homo sapiens.  
 OS  
 XX US5502176-A.  
 PN  
 PD 26-MAR-1996.  
 XX  
 PF 13-FEB-1992; 92US-0837776.  
 XX  
 PR 14-APR-1993; 93US-0049283.  
 PR 13-FEB-1992; 92US-0837776.  
 PR 19-FEB-1993; 93US-0020465.  
 XX  
 PA (BETH-) BETH ISRAEL HOSPITAL BOSTON ASSOC.  
 XX  
 PI Burn TC, Pahl HL, Tenen DG;  
 XX  
 DR WPI; 1996-179337/18.  
 XX  
 PT CD11b gene promoter directing gene expression pref. in myeloid cells  
 PT - directs expression in transient transfection assays in transgenic  
 PT animals, used to identify factors regulating myeloid cell-specific  
 PT transcription

XX Example 10; Column 25-26; 70pp; English.

XX An electrophoretic mobility shift assay (EMSA) was used to investigate  
 CC DNA/protein interactions in the CD11b promoter. Nuclear extracts from  
 CC U937 (myeloid) or HeLa (non-myeloid) cells were incubated with a 130 bp  
 CC probe which extends from bp -90 to +40 of the CD11b promoter. In  
 CC addition to the 130 bp probe, 30 bp double stranded oligonucleotides  
 CC were used as probes (AAT14576-79). The sequence between bp -64 and -59  
 CC constitutes a consensus binding site for the transcription factor Spl,  
 CC so to investigate whether complexes formed in the EMSA represent Spl  
 CC binding, a 97 bp DNA fragment of the tissue plasminogen promoter contg.  
 CC 2 characterised Spl binding sites was used as a competitor. The  
 CC complexes, but not the PU.1 complex, were competed by the addition  
 CC of DNA contg. Spl binding sites, indicating that they represent Spl  
 CC binding the CD11b promoter.

XX Sequence 30 BP; 2 A; 13 C; 5 G; 10 T; 0 other;  
 SQ

Query Match 64.0%; Score 12.8; DB 17; Length 30;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gggggagctcagtcgtg 19  
| | | | | | | | | | |  
DB 18 GCGGAGGCTCAGTGAG 3

RESULT 15  
AAT04232/c  
ID AAT04232 standard; DNA: 43 BP.  
XX  
AC AAT04232;  
XX  
DT 10-JAN-1996 (first entry)  
XX  
DE pNIV3606 amplification primer #1.  
XX  
KW Polymerase chain reaction; PCR; primer: amplify; histamine H1 receptor;  
KW human; bovine; transformation; drug screening; pNIV3604B;  
KW calcium ion mobilisation; inositol 1,4,5-triphosphate; CHO cell;  
KW guanine nucleotide regulatory protein; G protein; hybridisation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 14..43  
FT /\*tag= a  
FT /\*note= "corresponds to bases 1 to 48 of human histamine  
FT H1 DNA"

GB283239-A.  
XX  
PD 03-MAY-1995.  
XX  
PF 29-OCT-1993; 93GB-0022353.  
XX  
PR 29-OCT-1993; 93GB-0022353.  
XX  
PA (UNIO ) UCB SA.  
XX  
PI Bollen A, Gillard M, Moguilevsky N, Noyer M, Varsalona F;  
XX  
WPI; 1995-157301/21.

New nucleic acid encoding human histamine H1 receptor - useful  
diagnostically and for screening receptor binding drugs  
XX  
PS Example 3; Page 39; 49pp; English.

XX  
CC This sequence, and the sequence represented by AAT04233 are  
CC amplification primers for pNIV3606 (which contains human histamine H1  
CC receptor cDNA up to the fourth transmembrane region). The sequences shown  
CC in AAT04227, and AAT79965 represent human histamine H1 receptor cDNA and  
CC encoded receptor protein, and were constructed using AAT04234-6.  
CC Histamine H1 receptor is part of a family of histamine receptor proteins.  
CC Of these sequences the greatest homology was found with bovine histamine  
CC H1 receptor (overall identity of 82%, with the transmembrane regions  
CC alone having an identity of 96%). These receptors are coupled to  
CC different second messenger pathways via guanine nucleotide regulatory  
CC proteins (G proteins). This receptor transduces the signal through  
CC calcium ion mobilisation via an increase in intracellular inositol  
CC 1,4,5-triphosphate levels. Plasmids containing human histamine H1  
CC receptor cDNA (pref. pNIV3604B) are used to transform mammalian cells  
CC (pref. CHO cells). These transformed cells express the receptor on the  
CC cell surface. The transformed cells can then be used to identify ligands  
CC that bind to the encoded protein, esp. for drug screening. This sequence  
CC is also used to detect complementary mRNA in the cell by hybridisation.

XX  
SQ Sequence 43 BP; 10 A; 17 C; 4 G; 12 T; 0 other;

Query Match 64.0%; Score 12.8; DB 16; Length 43;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 taggggagggctcagtg 17  
| | | | | | | | | | |  
DB 27 TTGGGGAGGCTCATTG 12

Search completed: October 2, 2001, 16:18:44  
Job time: 15488 sec



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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run On: October 2, 2001, 16:03:50 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-15  
Perfect score: 20  
Sequence: 1 tgttggtttccaatcgacc 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCFUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-377-310-15
2	15	75.0	15	3	US-09-377-310-35
3	13.4	67.0	30	3	US-08-513-974B-129
C 4	12	60.0	30	1	US-08-295-676A-8
C 5	12	60.0	30	2	US-08-948-591-8
6	11.8	59.0	24	2	US-08-612-857-9
7	11.8	59.0	35	1	US-08-612-895A-29
8	11.8	59.0	35	3	US-09-093-293-29
9	11.8	59.0	35	5	PCT-US94-10562A-29
C 10	11.8	59.0	39	4	US-09-163-444-8
C 11	11.6	58.0	34	2	US-08-765-783A-42
C 12	11.6	58.0	34	3	US-08-921-100-42
C 13	11.6	58.0	34	3	US-08-880-142-42
C 14	11.6	58.0	34	3	US-08-902-201-42
C 15	11.6	58.0	34	4	US-09-416-557-42
C 16	11.6	58.0	41	3	US-08-813-507-97
17	11.4	57.0	28	2	US-08-859-998-979
18	11.2	56.0	24	4	US-08-855-146-12
C 19	11.2	56.0	25	3	US-09-085-603B-12
C 20	11.2	56.0	26	1	US-08-752-238-12
C 21	11.2	56.0	34	1	US-08-428-733A-47
C 22	11.2	56.0	37	2	US-08-873-479-54
C 23	11	55.0	18	3	US-09-163-162-19
C 24	11	55.0	18	4	US-09-286-407-19
C 25	11	55.0	21	1	US-08-266-080B-7
26	11	55.0	21	3	US-08-513-974B-262
27	11	55.0	21	3	US-08-513-974B-266

28 11 55.0 21 3 US-08-513-974B-271 Sequence 271, Appl  
 29 11 55.0 21 5 PCT-US95-05423-7 Sequence 7, Appli  
 30 11 55.0 23 4 US-09-268-140-29 Sequence 29, Appl  
 31 11 55.0 30 4 US-09-550-338-10 Sequence 10, Appl  
 C 32 11 55.0 31 1 US-08-656-984A-36 Sequence 36, Appl  
 C 33 11 55.0 33 3 US-08-468-846-7 Sequence 7, Appli  
 C 34 11 55.0 33 3 US-08-840-062-10 Sequence 10, Appl  
 C 35 11 55.0 36 1 US-07-937-609-12 Sequence 12, Appl  
 C 36 11 55.0 36 3 US-08-936-632B-38 Sequence 38, Appl  
 C 37 11 55.0 36 4 US-08-029-170-12 Sequence 12, Appl  
 C 38 11 55.0 36 4 US-08-582-333A-90 Sequence 90, Appl  
 C 39 11 55.0 40 1 US-08-443-957-7 Sequence 7, Appli  
 C 40 11 55.0 40 2 US-08-581-543-30 Sequence 30, Appl  
 C 41 11 55.0 45 1 US-08-171-382-10 Sequence 10, Appl  
 C 42 11 55.0 47 2 US-08-031-538-6 Sequence 6, Appli  
 C 43 10.8 54.0 30 3 US-08-513-974B-150 Sequence 150, App  
 C 44 10.8 54.0 31 1 US-08-450-384-8 Sequence 8, Appli  
 C 45 10.8 54.0 31 1 US-08-450-384-9 Sequence 9, Appli

## ALIGNMENTS

RESULT 1  
 US-09-377-310-15  
 ; Sequence 15, Application US/09377310B  
 ; Patent No. 6133031  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Monia, Brett P.  
 ; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
 ; FILE REFERENCE: ISPH-0389  
 ; CURRENT APPLICATION NUMBER: US/09/377,310B  
 ; CURRENT FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 15  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: antisense sequence  
 US-09-377-310-15

Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.035;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgttggtttccaatcgacc 20  
 |||

Db 1 tgttggtttccaatcgacc 20  
 |||

RESULT 2  
 US-09-377-310-35  
 ; Sequence 35, Application US/09377310B  
 ; Patent No. 6133031  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Monia, Brett P.  
 ; APPLICANT: Gaarde, William A.  
 ; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
 ; FILE REFERENCE: ISPH-0389  
 ; CURRENT APPLICATION NUMBER: US/09/377,310B  
 ; CURRENT FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 35  
 ; LENGTH: 15  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-35

Query Match 75.0%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ttggtttccaatcgg 17  
|||||  
Db 1 ttggtttccaatcgg 15

RESULT 3  
US-08-513-974B-129  
; Sequence 129, Application US/08513974B  
; Patent No. 6114139  
; GENERAL INFORMATION:  
; APPLICANT: Hinuma, Shuji  
; APPLICANT: Hosoya, Masaki  
; APPLICANT: Fujii, RYO  
; APPLICANT: Ohtaki, Tetsuya  
; APPLICANT: Fukusumi, Shoji  
; APPLICANT: Ohgi, Kazuhiko  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
; NUMBER OF SEQUENCES: 380  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,974B  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; PRIOR APPLICATION DATA: JP 7-093989  
; APPLICATION NUMBER: JP 7-093989  
; FILING DATE: 19-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-057186  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA: JP 7-007177  
; APPLICATION NUMBER: JP 7-007177  
; FILING DATE: 20-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-326611  
; FILING DATE: 28-DEC-1994  
; PRIOR APPLICATION DATA: JP 6-270017  
; APPLICATION NUMBER: JP 6-270017  
; FILING DATE: 02-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236357  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA: JP 6-236356  
; APPLICATION NUMBER: JP 6-236356  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189274  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189273

; FILING DATE: 11-AUG-1945  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189272  
; FILING DATE: 11-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 45753  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 129:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-513-974B-129  
  
Query Match 67.0%; Score 13.4; DB 3; Length 30;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 ttgttggtttccaatc 15  
|||||  
Db 10 TGTGTTTCCAAC 24  
  
RESULT 4  
US-08-295-676A-8/c  
; Sequence 8, Application US/08295676A  
; Patent No. 5677172  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: A method for production of proteins in  
; TITLE OF INVENTION: Yeast  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch and Birch  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/295,676A  
; FILING DATE: 09-SEPT-1994  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 5..10  
; OTHER INFORMATION: /function= "KpnI restriction site"  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..30  
; OTHER INFORMATION: /label= oligonucleotide  
; OTHER INFORMATION: /note= "synthetic 5' primer used to create  
; OTHER INFORMATION: recognition sites"  
US-08-295-676A-8

Query Match 60.0%; Score 12; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 6.6e+02;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tgttggtttccaatcgacc 20  
||||| ||| |||  
DB 24 TGTGTTCCAAAGGTACC 5

## RESULT 5

US-08-948-591-8/c  
Sequence 8, Application US/08948591  
Patent No. 5939287

## GENERAL INFORMATION:

APPLICANT: A method for production of proteins in  
TITLE OF INVENTION: Yeast  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch and Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,591

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/295,676

FILING DATE: 09-SEPT-1994

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: misc.feature

LOCATION: 5..10

OTHER INFORMATION: /function= "kpnI restriction site"

FEATURE:

NAME/KEY: -

LOCATION: 1..30

OTHER INFORMATION: /label= oligonucleotide

OTHER INFORMATION: /note= "synthetic 5' primer used to create

OTHER INFORMATION: recognition sites"

US-08-948-591-8

Query Match 60.0%; Score 12; DB 2; Length 30;  
Best Local Similarity 75.0%; Pred. No. 6.6e+02;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tgttggtttccaatcgacc 20  
||||| ||| |||  
DB 24 TGTGTTCCAAAGGTACC 5

## RESULT 6

US-08-612-857-9

Sequence 9, Application US/08612857

Patent No. 5831048

GENERAL INFORMATION:

APPLICANT: SCHWEIGHOFFER, Fabien

APPLICANT: TOCQUE, Bruno  
TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd. 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,857

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93-10971

FILING DATE: 15-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR94/00542

FILING DATE: 09-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: 38,619

REFERENCE/DOCKET NUMBER: ST93044-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)454-3839

TELEFAX: (610)454-3808

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "oligonucleotide IV"

US-08-612-857-9

Query Match

Best Local Similarity 59.0%; Score 11.8; DB 2; Length 24;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 tgggtttccaatcgga 18

DB 2 TCGTTTCCAAAGCGA 16

## RESULT 7

US-08-612-895A-29

Sequence 29, Application US/08612895A

Patent No. 5763177

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

APPLICANT: WILLIS, MICHAEL

APPLICANT: KOCH, TAD

APPLICANT: RINGQUIST, STEVEN

APPLICANT: JENSEN, KIRK

APPLICANT: ATKINSON, BRENT

TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF

TITLE OF INVENTION: LIGANDS BY EXPONENTIAL

TITLE OF INVENTION: ENRICHMENT: PHOTORESELECTION

TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND

TITLE OF INVENTION: SOLUTION SELEX

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG  
MEDIUM TYPE: storage  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,895A  
FILING DATE: 03 August 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10542  
FILING DATE: 18 September 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/123,935  
FILING DATE: 17 September 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/143,564  
FILING DATE: 25 October 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX10/PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-612-895A-29

Query Match 59.0%; Score 11.8; DB 1; Length 35;  
Best Local Similarity 40.0%; Pred. No. 8.7e+02;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgttggtttccaatc 15  
:|::|::|::|::|  
Db 18 UGUUUGUUCACUC 32

RESULT 8  
US-09-093-293-29  
Sequence 29, Application US/09093293  
Patent No. 6001577  
GENERAL INFORMATION:  
APPLICANT: GOLD, LARRY  
APPLICANT: WILLIS, MICHAEL  
APPLICANT: KOCH, TAD  
APPLICANT: RINGQUIST, STEVEN  
APPLICANT: JENSEN, KIRK  
APPLICANT: ATKINSON, BRENT  
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF  
TITLE OF INVENTION: LIGANDS BY EXPONENTIAL  
TITLE OF INVENTION: ENRICHMENT: PHOTORESELECTION  
TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND  
TITLE OF INVENTION: SOLUTION SELEX  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG

MEDIUM TYPE: storage  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,293  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,895  
FILING DATE: 03 August 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10542  
FILING DATE: 18 September 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/123,935  
FILING DATE: 17 September 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/143,564  
FILING DATE: 25 October 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10 JUNE 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11 JUNE 1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17 AUGUST 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX10/US-CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-093-293-29

Query Match 59.0%; Score 11.8; DB 3; Length 35;  
Best Local Similarity 40.0%; Pred. No. 8.7e+02;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgttggtttccaatc 15  
:|::|::|::|::|  
Db 18 UGUUUGUUCACUC 32

RESULT 9  
PCT-US94-10562A-29  
Sequence 29, Application PC/TUS9410562A  
GENERAL INFORMATION:  
APPLICANT: GOLD, LARRY  
APPLICANT: WILLIS, MICHAEL  
APPLICANT: KOCH, TAD  
APPLICANT: RINGQUIST, STEVEN  
APPLICANT: JENSEN, KIRK  
APPLICANT: ATKINSON, BRENT  
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF  
TITLE OF INVENTION: LIGANDS BY EXPONENTIAL  
TITLE OF INVENTION: ENRICHMENT: PHOTORESELECTION  
TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND  
TITLE OF INVENTION: SOLUTION SELEX  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200



CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10562A  
FILING DATE: 16 SEPTEMBER 1994  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/123,935  
FILING DATE: 17 September 1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/143,564  
FILING DATE: 25 October 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX10/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US94-10562A-29

Query Match 59.0%; Score 11.8; DB 5; Length 35;  
Best Local Similarity 40.0%; Pred. No. 8.7e+02;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgggtgttccaatc 15  
DB 18 UGUUGUUGUCCACUC 32

RESULT 10  
US-09-163-444-8/c  
; Sequence 8, Application US/09163444  
; Patent No. 6251596  
; GENERAL INFORMATION:  
; APPLICANT: Cook, James W.  
; APPLICANT: Bulawa, Christine  
; TITLE OF INVENTION: ASPERGILLUS N-MYRISTOYL TRANSFERASE GENES AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 07334/089001  
; CURRENT APPLICATION NUMBER: US/09/163,444  
; CURRENT FILING DATE: 1998-09-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Aspergillus fumigatus N-myrystoyl  
US-09-163-444-8

Query Match 59.0%; Score 11.8; DB 4; Length 39;  
Best Local Similarity 86.7%; Pred. No. 8.8e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gttgtttccaatcg 16  
DB 34 GTTGTTCCTCAATAG 20

## RESULT 11

US-08-765-783A-42/c  
; Sequence 42, Application US/08765783A  
; Patent No. 5994524  
; GENERAL INFORMATION:  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Matsumoto, Yoshihiro  
; APPLICANT: Yamada, Yoshiki  
; APPLICANT: Sato, Koh  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yamazaki, Tatsumi  
; TITLE OF INVENTION: Reshaped Human Antibody to  
; INTERLEUKIN-8  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,783A  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 35029-20001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0169  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1...34  
; OTHER INFORMATION: LTW1 sequence  
US-08-765-783A-42

Query Match 58.0%; Score 11.6; DB 2; Length 34;  
Best Local Similarity 77.8%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ttgggttccaatcgacc 20  
DB 32 TTTGTTTCTTAATGAGACC 15

## RESULT 12

US-08-921-100-42/c  
; Sequence 42, Application US/08921100  
; Patent No. 6024956  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI

```

; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,100
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,323
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-921-100-42

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Query Match      58.0%; Score 11.6; DB 3; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 3 ttggtttccaatcgacc 20
   ||||| ||| ||||
DB 32 TTTGTTTCTAATGAGACC 15

```

```

RESULT 13
US-08-880-142-42/c
; Sequence 42, Application US/08880142
; Patent No. 6048972
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI
; APPLICANT: MATSUMOTO, YOSHIHIRO
; APPLICANT: YAMADA, YOSHIKI
; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,201
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,328
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,142
; FILING DATE: 20-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/345,145
; FILING DATE: 28-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-880-142-42

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Query Match      58.0%; Score 11.6; DB 3; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 3 ttggtttccaatcgacc 20
   ||||| ||| ||||
DB 32 TTTGTTTCTAATGAGACC 15

```

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RESULT 14
US-08-902-201-42/c
; Sequence 42, Application US/08902201
; Patent No. 6068840
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI
; APPLICANT: MATSUMOTO, YOSHIHIRO
; APPLICANT: YAMADA, YOSHIKI
; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,201
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,328
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500

```

TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-902-201-42

Query Match 58.0%; Score 11.6; DB 3; Length 34;  
Best Local Similarity 77.8%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ttggtttccaatcgacc 20  
||| ||||| ||| |||||  
Db 32 TTGTTTCTAATGAGACC 15

RESULT 15

US-09-416-557-42/c  
; Sequence 42, Application US/09416557  
; Patent No. 6245894  
; GENERAL INFORMATION:  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Matsumoto, Yoshihiro  
; APPLICANT: Yamada, Yoshiki  
; APPLICANT: Sato, Koh  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yamazaki, Tatsumi  
; TITLE OF INVENTION: Reshaped Human Antibody to  
; TITLE OF INVENTION: Interleukin-8  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/416,557  
; FILING DATE: 12-October-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,783  
; FILING DATE: 7-March-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 35029-20001.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0168  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1...34  
; OTHER INFORMATION: LTw1 sequence

US-09-416-557-42

Query Match 58.0%; Score 11.6; DB 4; Length 34;  
Best Local Similarity 77.8%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3 ttggtttccaatcgacc 20  
||| ||||| ||| |||||  
Db 32 TTGTTTCTAATGAGACC 15

Search completed: October 2, 2001, 16:03:51  
Job time: 14595 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:42 ; Search time 876.95 Seconds  
(without alignments)  
14.320 Million cell updates/sec

Title: US-09-757-100B-15  
Perfect score: 20  
Sequence: 1 tgggtgttccaatcgacc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0601.\*  
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2: /SIDS8/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SIDS8/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SIDS8/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SIDS8/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SIDS8/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SIDS8/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SIDS8/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SIDS8/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SIDS8/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
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16: /SIDS8/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SIDS8/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SIDS8/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SIDS8/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	22	AA65547 Human focal adhesi
2	15	75.0	15	22	AA65567 Human focal adhesi
3	13	65.0	19	14	AAQ48576 HPV E6/7 region pr
4	12.6	63.0	35	21	AAAL2990 Cellulomonas fimi
5	12.6	63.0	35	21	AAZ54999 Neisseria species
6	12.6	63.0	43	11	AAQ04950 Oligonucleotide ca
7	12.4	62.0	17	21	AAA36501 Human genomic SNP
8	12.4	62.0	21	21	AAZ99639 Nucleotide sequenc
9	12.4	62.0	24	22	AA66935 Arabidopsis AOXIA
10	12.2	61.0	17	20	AAV93672 Human B-raf substr
11	12.2	61.0	20	16	AAQ95843 Primer A (Group 11

c 12	12.2	61.0	28	19	AAV23724	PCR primer used in
c 13	12.2	61.0	32	20	AAZ21962	Primer BB10 for hu
c 14	12.2	61.0	32	21	AAZ74774	E. coli still signa
c 15	12.2	61.0	34	21	AAZ74783	Human growth hormo
c 16	12.0	60.0	20	20	AAZ96260	PCR primer used to
c 17	12.0	60.0	24	21	AAA40065	Rice disease resis
c 18	12.0	60.0	26	20	AAZ82064	Streptococcus pneu
c 19	12.0	60.0	30	14	AAQ48878	Neurotrophic facto
c 20	12.0	60.0	33	18	AAZ60126	Coding sequence fo
c 21	12.0	60.0	38	21	AAZ55244	Paenibacillus oxid
c 22	12.0	60.0	41	19	AAV50662	Brassica sp. polym
c 23	12.0	60.0	41	19	AAV50663	Brassica sp. polym
c 24	12.0	60.0	42	20	AAZ09476	pl35-NT5C construc
c 25	11.8	59.0	22	22	AAZ55629	PCR primer for Syb
c 26	11.8	59.0	24	16	AAQ89216	Grb3-3 gene PCR 3'
c 27	11.8	59.0	26	21	AAZ63754	Maize cytotypospe
c 28	11.8	59.0	30	21	AAZ72212	Aspergillus oryzae
c 29	11.8	59.0	34	21	AAA12988	Streptomyces oliva
c 30	11.8	59.0	35	16	AAQ83604	Human immunodifici
c 31	11.8	59.0	35	22	AAZ72349	3' PCR primer spec
c 32	11.8	59.0	44	21	AAZ64475	Plasmid pCLYV con
c 33	11.6	58.0	19	21	AAZ84286	Cyclin D1 ribozyme
c 34	11.6	58.0	25	16	AAZ02563	Heat shock protein
c 35	11.6	58.0	27	21	AAZ39578	M. tuberculosis an
c 36	11.6	58.0	30	16	AAQ80608	Primer 5WK for IgE
c 37	11.6	58.0	34	17	AAZ16952	Human/murine chima
c 38	11.6	58.0	34	20	AAZ91952	Porphorymonas ging
c 39	11.6	58.0	42	21	AAZ94784	hla gene PCR prime
c 40	11.6	58.0	42	21	AAZ99009	H. influenzae adhe
c 41	11.6	58.0	42	21	AAZ65067	Exemplary DNA #5 e
c 42	11.6	58.0	50	18	AAZ79498	Staphylococcus aur
c 43	11.6	58.0	50	20	AAZ85630	Novel cDNA sequenc
c 44	11.4	57.0	17	20	AAZ91187	Human C-raf target
c 45	11.4	57.0	20	20	AAZ03515	PCR primer used to

ALIGNMENTS

RESULT 1  
AAC65547  
ID AAC65547 standard; DNA; 20 BP.  
XX  
AC AAC65547;  
XX  
DT 12-FEB-2001 (first entry)  
XX  
DE Human focal adhesion kinase antisense sequence #13.  
XX  
KW Human; focal adhesion kinase; FAK; signal transduction; cancer;  
KW embryonic development disorder; angiogenic disorder; wound healing;  
KW antisense; phosphorothioate; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6133031-A.  
XX  
PD 17-OCT-2000.  
XX  
PF 19-AUG-1999; 99US-0377310.  
XX  
PR 19-AUG-1999; 99US-0377310.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Gaarde WA;  
XX  
DR WPI; 2001-006141/01.  
XX  
PT New antisense compounds for inhibiting focal adhesion kinase  
PT expression, especially useful for inhibiting retinal  
PT neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Claim 15; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
CC is involved in integrin-mediated signal transduction, and is implicated  
CC in cancer, particularly colon, breast and oral tumours, embryonic  
CC development disorders, angiogenic disorders and wound healing. The  
CC antisense sequences, including the one shown here, can be used in the  
CC treatment of all of these.

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgggtgttccaatcgacc 20  
|||||  
Db 1 tgggtgttccaatcgacc 20

RESULT 2

AAC65567  
ID AAC65567 standard; DNA; 15 BP.

AC AAC65567;

XX 12-FEB-2001 (first entry)

XX Human focal adhesion kinase antisense sequence #33.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;  
KW embryonic development disorder; angiogenic disorder; wound healing;  
KW antisense; phosphorothioate; ss.

XX Homo sapiens.

XX US6133031-A.

XX 17-OCT-2000.

PF 19-AUG-1999; 99US-0377310.

PR 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase  
PT expression, especially useful for inhibiting retinal  
PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX Example 2; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense  
CC sequences to the human focal adhesion kinase (FAK) protein. This protein  
CC is involved in integrin-mediated signal transduction, and is implicated  
CC in cancer, particularly colon, breast and oral tumours, embryonic  
CC development disorders, angiogenic disorders and wound healing. The  
CC antisense sequences, including the one shown here, can be used in the  
CC treatment of all of these.

XX Sequence 15 BP; 2 A; 3 C; 4 G; 6 T; 0 other;

Query Match 75.0%; Score 15; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 66; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ttggtttccaatcgg 17  
|||||  
Db 1 ttggtttccaatcgg 15

RESULT 3

AAQ48576/c  
ID AAQ48576 standard; DNA; 19 BP.

XX AC AAQ48576;

XX 22-FEB-1994 (first entry)

XX HPV E6/7 region probe.

XX Human papilloma virus; HPV; E6; E7; benign; malignant; probe; ss.

XX Synthetic.

XX JP05192200-A.

XX 03-AUG-1993.

PF 19-AUG-1991; 91JP-0230839.

PR 20-AUG-1990; 90JP-0217067.

XX (TAKI ) TAKARA SHUZO CO LTD.

XX WPI; 1993-277497/35.

XX Detecting benign and/or malignant human papilloma virus - by  
PT detecting DNA sequence of E6 and/or E7 region of human papilloma  
PT virus

XX Disclosure; Page 17; 18pp; Japanese.

XX The probe is used to detect benign and/or malignant human papilloma  
CC virus. The probe binds to the E6 and/or E7 region of the virus.

XX Sequence 19 BP; 7 A; 4 C; 5 G; 3 T; 0 other;

Query Match 65.0%; Score 13; DB 14; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.6e-02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgggtgttccaa 13  
|||||  
Db 14 TGTGTGTTCCAA 2

RESULT 4

AAA12990  
ID AAA12990 standard; DNA; 35 BP.

XX AC AAA12990;

XX 18-JUL-2000 (first entry)

XX Cellulomonas fimi xylanase PCR primer, SEQ ID NO:6.

XX Xylanase; endo-1,4-beta-xylanase; xylan hydrolysis;

XX xylo-oligosaccharide production; chimeric xylanase; PCR primer; ss.

XX Cellulomonas fimi.

XX JP3030331-B1.

XX 10-APR-2000.

PF 17-MAR-1999; 99JP-0071715.

PR 17-MAR-1999; 99JP-0071715.  
 XX (NORQ ) NORIN-SUISANSHO SHOKUHIN SOGO KENKYUSHOCHO.  
 PA (SEIB-) SEIBUTSUKETI TOKUTEI SANGYO GIJUTSU KENKYU SUISHIN KIKO.  
 XX  
 DR WPI: 2000-306509/27.  
 XX  
 PT Modified xylanase gene for use in foodstuff industry, has base sequence  
 PT of 1065 nucleotides -  
 XX  
 XX Example 1; Page 10; 11pp; Japanese.  
 PS  
 XX The invention relates a novel chimeric xylanase (AA12985) and to DNA  
 CC encoding it (AA12985). The chimeric xylanase comprises residues 1-244  
 CC of Streptomyces olivaceoviridis xylanase and residues 244-354 of  
 CC Cellulomonas fimi xylanase. Xylanase (also known as endo-1,4-beta-  
 CC xylanase) hydrolyses beta-1,4-D-xylan, a component of the hemicellulose  
 CC in plant cell walls, into xylo-oligosaccharides and xylose. Xylanase is  
 CC used in a range of industrial processes. It is used to produce xylo-  
 CC oligosaccharides from xylan from broad-leaved trees, and is used in  
 CC wood- pulp bleaching to reduce the amount of chlorine required for this  
 CC process. Xylo-oligosaccharides can be used as ingredients in foodstuffs  
 CC and as water-retaining material in cosmetics. The chimeric xylanase of  
 CC the invention does not generate xylose monomers during the hydrolysis of  
 CC xylan. It is therefore useful for efficient and reliable xylo-  
 CC oligosaccharide production. Sequences AA12990-AA12991 represent PCR  
 CC primers used in an exemplification of the present invention to amplify  
 CC a portion of the Cellulomonas fimi xylanase gene encoding residues  
 CC 244-354 of the protein. The PCR product was then used to generate  
 CC DNA encoding the chimeric xylanase via a second round of PCR using  
 CC primers AA12987 and AA12991.  
 XX  
 SQ Sequence 35 BP; 3 A; 15 C; 9 G; 8 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 35;  
 Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 gttgtttccaatcgacc 20  
 ||||| ||||| ||||| |||||  
 Db 5 gtcggcttcacgacgcacc 23

RESULT 5  
 AAZ54999/C  
 ID AAZ54999 standard; DNA; 35 BP.  
 XX  
 AC AAZ54999;

DT 21-MAR-2000 (first entry)  
 XX  
 DE Neisseria species ORF cloning PCR primer #384.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;  
 KW antibacterial; gene therapy; PCR primer; ss.

OS Synthetic.  
 OS Neisseria sp.  
 XX  
 XX WO9957280-A2.  
 PN  
 XX  
 XX 11-NOV-1999.

PF 30-APR-1999; 99WO-US09346.

XX  
 PR 01-MAY-1998; 98US-0083758.  
 PR 31-JUL-1998; 98US-0094869.  
 PR 02-SEP-1998; 98US-0098994.  
 PR 02-SEP-1998; 98US-0099062.  
 PR 09-OCT-1998; 98US-0103749.  
 PR 09-OCT-1998; 98US-0103794.

PR 09-OCT-1998; 98US-0103796.  
 PR 25-FEB-1999; 99US-0121528.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
 PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
 PI Tettelin H, Venter JC;  
 XX  
 DR WPI: 2000-062150/05.  
 XX  
 PT Novel Neisserial polypeptides predicted to be useful antigens for  
 PT vaccines and diagnostics -  
 XX  
 PS Example 16; Page 150; 1453pp; English.  
 XX  
 CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAZ74253 to AAZ75941  
 CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides  
 CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of  
 CC the invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the  
 CC manufacture of medicaments for treating or preventing infection due to  
 CC Neisserial bacteria (e.g. meningitis and septicaemia), to detect the  
 CC presence of Neisseria bacteria, or to raise antibodies. They may also  
 CC be used to screen for agonists or antagonists, which may themselves  
 CC have use as antibacterial agents. The polynucleotides of the invention  
 CC may also be used in gene therapy protocols.  
 XX  
 SQ Sequence 35 BP; 18 A; 5 C; 7 G; 5 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 35;  
 Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tttgttttccaatcgacc 19  
 ||||| ||||| ||||| |||||  
 Db 32 TGTGTGTTTTCATCAGCC 14

RESULT 6  
 AAQ04950  
 ID AAQ04950 standard; DNA; 43 BP.  
 XX  
 AC AAQ04950;

DT 24-OCT-1990 (first entry)  
 XX  
 DE Oligonucleotide carrying mutation for factor V gene.

XX Human factor VIII analogue; ss.

OS Synthetic.

FH Key Location/Qualifiers  
 FT mutation 19..24  
 FT /\*tag= a

XX WO9005530-A.

XX PN  
 XX 31-MAY-1990.

XX PF 14-NOV-1989; 89WO-0005049.

XX PR 14-NOV-1988; 88US-0270882.

XX PA (GENE-) GENETICS INST INC.

XX KA Kaufman RJ, Pittman DD;

XX

DR WPI; 1990-193265/25.  
XX New hybrid DNA encoding hybrid procoagulant proteins -  
PT prep'd. by modifying DNA encoding human factor VIII.  
XX  
XX  
PS Disclosure; ; pp; English.  
XX  
XX Factor VIII analogue is sufficiently mutated from the original gene  
CC that it is not recognised by blood Abs of the patient. The analogue  
CC is composed of human FVIII but carries the B-domain of human FV in  
CC place of the FVIII B-domain.  
CC Oligonucleotides can be used to alter the profile of the blood  
CC factor without significantly altering its activity.  
XX  
XX Sequence 43 BP; 10 A; 10 C; 11 G; 12 T; 0 other;  
SQ

Query Match 63.0%; Score 12.6; DB 11; Length 43;  
Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
AC

QY 1 tgttggtttccaatcgac 19  
||||| ||||| |||||  
Db 25 tgtaggatgccaatgggac 43

RESULT 7  
AAA36501  
ID AAA36501 standard; DNA; 17 BP.  
XX  
AC AAA36501;  
XX  
XX 26-JUL-2000 (first entry)  
DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:566.  
XX  
XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;  
KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;  
KW genomic classification; identification; DNA fingerprinting;  
KW tumour characterisation; hybridisation; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200018960-A2.  
PN  
XX  
XX 06-APR-2000.  
PD  
XX  
XX 24-SEP-1999; 99WO-US22283.  
PF  
XX  
XX 25-SEP-1998; 98US-0101757.  
PR  
XX  
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA  
XX  
XX Landers JE, Jordan B, Housman DE, Charest A;  
PI  
XX WPI; 2000-293181/25.  
DR

Detection of single nucleotide polymorphisms in genomes by preparation  
PT and analysis of reduced complexity genomes, useful for genotyping,  
PT fingerprinting and determining allele frequency of SNPs -  
XX  
XX Disclosure; Page 70; 111pp; English.  
XX

A method has been developed for detecting the presence or absence of a  
CC single nucleotide polymorphism (SNP) allele in a genomic sample. The  
CC method comprises preparing a reduced complexity genome (RCG) from the  
CC genomic sample and analysing the RCG for the presence or absence of a  
CC SNP allele. The method can be used to characterise a tumour, to generate  
CC a genomic pattern for an individual genome or to generate a genomic  
CC classification code for a genome. The method can be used to assess  
CC whether a subject is at risk for developing a disease or to identify a  
CC set of SNP alleles associated with a disease. The method can also be  
CC used to perform linkage analysis. AAA35944 to AAA35947 represent

sequences used in the exemplification of the present invention. AAA35948  
CC to AAA36532 represent nucleotide sequences containing SNPs.  
XX  
XX Sequence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 other;  
SQ

Query Match 62.0%; Score 12.4; DB 21; Length 17;  
Best Local Similarity 92.9%; Pred. No. 1.6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
AC

QY 5 ggtttccaatcgga 18  
||||| ||||| |||||  
Db 1 ggtttccaatggga 14

RESULT 8  
AAZ99639  
ID AAZ99639 standard; DNA; 21 BP.  
XX  
AC AAZ99639;  
XX  
XX 12-JUL-2000 (first entry)  
DE Nucleotide sequence of G-motif oligonucleotide P2314.  
XX

G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;  
KW antigen presenting cell activation; natural killer cell; septic shock;  
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;  
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;  
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;  
KW helper T cell response 1-mediated disease; Lyme arthritis;  
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;  
KW psoriasis vulgaris; experimental allergic encephalomyelitis;  
KW insulin-dependent diabetes mellitus; bacterial infection;  
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.  
XX  
XX Synthetic.  
OS  
XX WO200014217-A2.  
PN  
XX 16-MAR-2000.  
PD  
XX  
XX 03-SEP-1999; 99WO-EP06502.  
PF  
XX  
XX 03-SEP-1998; 98EP-0116852.  
PR  
XX  
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.  
PA  
XX  
XX Wagner H, Lipford GB, Heeg K;  
PI  
XX WPI; 2000-256970/22.  
DR

Compositions comprising G-motif oligonucleotides useful for treating  
PT e.g. septic shock, rheumatoid arthritis, diabetes and human  
PT immunodeficiency virus infections -  
XX  
XX Disclosure; Page 34; 75pp; English.  
XX

The present sequence represents a G-motif oligonucleotide of the  
CC invention. The specification describes compositions comprising G-motif  
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of  
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by  
CC stimulating natural killer cells, or by co-stimulating cytotoxic  
CC T-lymphocytes. The G-motif oligonucleotides may be used for the  
CC productions of vaccines for treating septic shock, inflammation,  
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,  
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host  
CC disease and transplant rejection), helper T cell response 1-mediated  
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic  
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic  
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus



CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
 CC used to induce proliferation of bone marrow cells, especially macrophage  
 CC precursor cells.

XX Sequence 21 BP; 2 A; 5 C; 3 G; 11 T; 0 other;

Query Match 62.0%; Score 12.4; DB 21; Length 21;  
 Best Local Similarity 92.9%; Pred. No. 1.6e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgggtgttcacat 14  
 |||||  
 Db 8 tgggtgttcacat 21

RESULT 9  
 AAC66935  
 ID AAC66935 standard; DNA; 24 BP.

XX  
 AC AAC66935;

XX 27-MAR-2001 (first entry)

XX Arabidopsis AOXla gene promoter PCR primer #2.

XX Plant signal transduction pathway; reporter vector;  
 KW luciferase; herbicide resistance; pest resistance; PCR primer; ss.

XX Arabidopsis thaliana.

XX WO200071668-A2.

XX 30-NOV-2000.

XX 22-MAY-2000; 2000WO-US14041.

XX 20-MAY-1999; 99US-0136145.

XX (UYNE-) UNIV NEBRASKA.

XX Rhoades DM;

XX WPI; 2001-025143/03.

XX Identifying genes encoding signal transduction components useful for  
 PT producing transgenic plants, by transforming plants with vector  
 PT encoding reporter gene, mutating the plant and identifying genes from  
 PT the mutant

XX Example 1; Page 54; 54pp; English.

XX The present invention provides a method for identifying genes encoding  
 CC components of plant signal transduction pathways between mitochondrial  
 CC function and metabolic status and nuclear gene expression. This involves  
 CC the transformation of a plant with a vector encoding a reporter gene  
 CC linked to an AOX promoter, mutagenesis of the plant to increase  
 CC expression of the reporter gene and then determining the identity of the  
 CC signal transduction gene of interest. This is useful in the production of  
 CC transgenic plants with increased productivity, herbicide, stress and pest  
 CC resistance.

XX Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;

Query Match 62.0%; Score 12.4; DB 22; Length 24;  
 Best Local Similarity 92.9%; Pred. No. 1.6e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 tgggttcacatcg 17  
 |||||  
 Db 11 tgggttcacatcg 24

RESULT 10  
 AAV93672

ID AAV93672 standard; RNA; 17 BP.

XX  
 AC AAV93672;

XX 18-FEB-1999 (first entry)

XX Human B-raf substrate nucleotide position 2272.

XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene;  
 KW delivery; screening; identification; synthesis; deprotection;  
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;  
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.

XX Homo sapiens.

XX WO9850530-A2.

XX 12-NOV-1998.

XX 05-MAY-1998; 98WO-US09249.

XX 19-DEC-1997; 97US-0068212.

XX 09-MAY-1997; 97US-0046059.

XX 09-JUN-1997; 97US-0049002.

XX 03-JUL-1997; 97US-0051718.

XX 22-AUG-1997; 97US-0056808.

XX 02-OCT-1997; 97US-0061321.

XX 02-OCT-1997; 97US-0061324.

XX 05-NOV-1997; 97US-0064866.

XX (RIBO-) RIBOZYME PHARM INC.

XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;

XX Karpeisky A, Kisich K, Matulic-Adamic J, McSwigen JA;

XX Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;

XX WPI; 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected

XX processes - especially ribozymes that cleave Raf RNA for treating

XX cancer, restenosis, and also new ribozymes and modified nucleoside

XX triphosphates used as antiviral agents and synthons

XX Claim 177; Page 172; 259pp; English.

XX A method has been developed for the identification of a nucleic acid

XX capable of modulating a process in a biological system. The method

XX comprises: (a) introducing into the system a random library of nucleic

XX acid catalysts (NAC) having a substrate binding domain (SBD), comprising

XX a random sequence, and a catalytic domain (CD); and (b) identifying NAC

XX in systems where modulation has occurred and/or determining the sequence

XX of at least part of the SBDs in such systems. Nucleic acid molecules

XX with endonuclease activity and catalytic activity, from the present

XX invention, are used to modulate gene expression in plant and mammalian

XX cells and to cleave target nucleic acid, particularly for treating

XX systemic diseases caused by specific RNA, e.g. cancer, inflammation,

XX psoriasis, non-hepatic ascites and infection. They may also be used to

XX detect genetic drift and mutations in diseased cells and to determine

XX c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate

XX expression of the Raf gene, are used to treat cancer, restenosis,

XX psoriasis or rheumatoid arthritis, or generally any condition associated

XX with the level of c-raf. Introduction of sugar/phosphate modifications

XX increases stability against nuclease and activity. AAV90922 to AAV93877

XX represent NACs that can be used in the method, specifically for

XX modulating the expression of a Raf gene.

XX Sequence 17 BP; 5 A; 4 C; 4 G; 4 U; 0 other;

Query Match 61.0%; Score 12.2; DB 20; Length 17;  
 Best Local Similarity 58.8%; Pred. No. 2e+03;  
 Matches 10; Conservative 4; Mismatches 0; Gaps 0;

QY 2 gtgtgtttccaatcgga 18  
 | :|||:|||| | |  
 Db 1 gcugguuuccaacaaga 17

RESULT 11  
 AAQ95843  
 ID AAQ95843 standard; DNA; 20 BP.  
 XX AC AAQ95843;  
 XX XX  
 DT 21-FEB-1996 (first entry)  
 XX XX  
 DE Primer A (Group 11, set A) for marker D9S180, chromosome 9.  
 XX XX  
 KW primer; polymerase chain reaction; PCR; linkage study; locus;  
 KW microsatellite marker sequence; automated genotyping; allele;  
 KW polymorphism; detection; Homo sapiens; ss.  
 XX XX  
 OS Synthetic.  
 XX XX  
 PN WO9515400-AL.  
 XX XX  
 PD 08-JUN-1995.  
 XX XX  
 PF 05-DEC-1994; 94WO-US13945.  
 XX XX  
 PR 03-DEC-1993; 93US-0160837.  
 XX XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX XX  
 PI Levitt RC;  
 XX XX  
 DR WPI; 1995-215278/28.  
 XX XX  
 PT Kit for automated genotyping contg. pairs of PCR primers - designed  
 PT to amplify polymorphic nucleotide repeat sequences, arranged in sets  
 PT each with a characteristic fluorescence label, useful e.g. in  
 PT detection of disease related genetic rearrangement  
 XX XX  
 PS Disclosure; Fig 7K-2; 104pp; English.  
 XX XX  
 CC The method aims to provide a collection of highly reproducible  
 CC microsatellite marker sequences (MMS) at approx. 10-50 cm intervals  
 CC throughout the human genome which can be detectably labelled. The  
 CC MMS are polymorphic, simple sequence repeats and can be used in  
 CC automated genotyping. esp. fluorescence-based. The primers correspond  
 CC to the unique DNA sequence surrounding each marker, and PCR is used to  
 CC detect each polymorphism. When the MMS show considerable polymorphism  
 CC (ie. a difference in the number of repeats) between individuals, the  
 CC markers can be particularly informative. The MMS can be ideal for  
 CC linkage studies. Kits comprise at least 4 groups, of at least 3 sets,  
 CC each comprising labelled primers for PCR amplification of the DNA.  
 CC Group 11 primer pairs are shown in AAQ95841-82. The published size range  
 CC of the D9S180 allele is 220-265 bp, and the degree of heterozygosity  
 CC in the population is about 63%.  
 XX XX  
 SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Query Match 61.0%; Score 12.2; DB 16; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 2e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tgggtttccaatcggaac 20  
 | ||||| ||||| ||  
 Db 4 tgggttggaaatcggaac 20

RESULT 12  
 AAV23724/c  
 ID AAV23724 standard; DNA; 28 BP.  
 XX AC AAV23724;  
 XX XX  
 DT 20-AUG-1998 (first entry)  
 XX XX  
 DE PCR primer used in the course of the invention.  
 XX XX  
 KW Lipase; variant; improved wash performance; removal; lipid stain;  
 KW reduced calcium dependence; one-cycle wash efficiency; detergent;  
 KW cleaning composition; PCR primer; ss.  
 XX XX  
 OS Synthetic.  
 OS Pseudomonas pseudoalcaligenes.  
 XX PN WO9808939-AL.  
 XX XX  
 PD 05-MAR-1998.  
 XX XX  
 PF 26-AUG-1997; 97WO-DK00345.  
 XX XX  
 PR 29-AUG-1996; 96US-0029190.  
 PR 27-AUG-1996; 96DK-0000902.  
 XX XX  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX XX  
 PI Okkels JS, Svendsen A;  
 XX XX  
 DR WPI; 1998-230259/20.  
 XX XX  
 PT Variants of lipase from pseudomonas containing specific amino acid  
 PT substitutions - deletions or additions, having improved wash  
 PT performance in detergent formulations  
 XX XX  
 PS Disclosure; Page 75; 104pp; English.  
 XX XX  
 CC PCR primers AAV23717-32 were used during the course of the invention.  
 CC The specification describes Pseudomonas pseudoalcaligenes lipase  
 CC variants. The variant lipases described in the specification has have  
 CC better wash performance than the original lipase. It has improved  
 CC removal of lipid stains, reduced calcium dependence, better compatibility  
 CC with detergents or their components, increased hydrophobicity, altered  
 CC substrate specificity and better one-cycle wash efficiency. The variant  
 CC lipase is used in detergent and cleaning compositions.  
 XX XX  
 SQ Sequence 28 BP; 7 A; 7 C; 8 G; 6 T; 0 other;

Query Match 61.0%; Score 12.2; DB 19; Length 28;  
 Best Local Similarity 82.4%; Pred. No. 2.1e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ttgtgtttccaatcggaac 19  
 | ||||| | | | |  
 Db 21 TTGGTTTCGAACCGAAC 5

RESULT 13  
 AAX21962/c  
 ID AAX21962 standard; DNA; 32 BP.  
 XX AC AAX21962;  
 XX XX  
 DT 18-MAY-1999 (first entry)  
 XX XX  
 DE Primer BB10 for human growth hormone gene.  
 XX XX  
 KW PCR primer; human; growth hormone; variant; cachexia; erythropoietin;  
 KW erythrocyte formation; interferon; antiviral; antitumour; interleukin;  
 KW immunomodulatory agent; colony-stimulating factor;  
 KW proliferation stimulation; ss.

XX Synthetic.  
OS Homo sapiens.  
XX WO9903887-A1.  
PN  
XX  
PD 28-JAN-1999.  
XX  
XX 13-JUL-1998; 98WO-US14497.  
PF  
XX 14-JUL-1997; 97US-0052516.  
PR  
XX  
PA (BOLD-) BOLDER BIOTECHNOLOGY INC.  
XX  
XX Cox GN;  
PI  
XX WPI; 1999-132163/11.  
DR  
XX New variants of growth hormone superfamily proteins containing an  
PT extra cysteine - useful, e.g. for treatment of short stature or  
PT cachexia, to stimulate erythrocyte formation and as immunomodulator  
XX  
PS Example 1; Page 16; 94pp; English.  
XX  
CC This sequence is a PCR primer for the human growth hormone gene. The  
CC invention relates to a variant of a member of the growth hormone (GH)  
CC superfamily that has a Cys residue: (a) replacing an amino acid (aa) in  
CC the loop regions, near the end of the alpha-helices or in front of, or  
CC after, the first amphipathic helix; (b) added to the N- or C- terminus;  
CC or (c) introduced between two aa in the loop region, at the ends of the  
CC alpha-helices or in front of, or after, the first amphipathic helix. The  
CC variants are used for the same therapeutic purposes as the wild type  
CC sequences, e.g. for GH to treat short stature or cachexia; for  
CC erythropoietin (EPO) to stimulate erythrocyte formation; for interferons  
CC as antiviral, antitumour or immunomodulatory agents; for  
CC colony-stimulating factors or interleukins for stimulating proliferation,  
CC differentiation and function of particular types of (haematopoietic)  
CC cells. Incorporation of Cys at a non-essential position allows  
CC site-specific attachment of e.g. poly(ethylene glycol) (PEG) to create a  
CC conjugate with increased circulation time in vivo. This reduces the need  
CC for frequent injections and the cost of treatment. Modification with PEG  
CC also increases solubility and stability of the protein and reduces its  
CC immunogenicity.  
XX  
SQ Sequence 32 BP; 7 A; 13 C; 6 G; 6 T; 0 other;

Query Match 61.0%; Score 12.2; DB 20; Length 32;  
Best Local Similarity 82.4%; Pred. No. 2.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tgggttcgaatcgacc 20  
||| ||| ||| ||| |||  
Db 21 TGGATTCTAATCGGATC 5

RESULT 14  
AAA74774/c  
ID AAA74774 standard; DNA; 32 BP.  
XX  
AC AAA74774;  
XX  
DT 17-JAN-2001 (first entry)  
XX  
DE E. coli stII signal sequence PCR primer BB10.  
XX  
XX Erythropoietin; growth hormone; IFN-alpha2; free cysteine residue;  
KW PCR primer; ss.  
XX  
XX Escherichia coli.  
OS  
XX WO200042175-A1.  
PN  
XX

PD 20-JUL-2000.  
XX  
XX 14-JAN-2000; 2000WO-US00931.  
PF  
XX 14-JAN-1999; 99US-0116041.  
PR  
XX (BOLD-) BOLDER BIOTECHNOLOGY INC.  
PA  
XX Cox GN, Doherty DH, Rosendahl MS;  
PI  
XX WPI; 2000-476056/41.  
DR  
XX Producing a soluble protein having a free cysteine comprises exposing a  
PT host cell expressing the soluble protein to a cysteine blocking agent,  
PT useful for producing recombinant human growth factor and erythropoietin  
PT .  
XX  
PS Example 2; Page 18; 86pp; English.  
XX  
CC The present invention concerns novel methods of producing proteins with  
CC free cysteine residues. The PCR primers AAA74770-A74854 were used to  
CC amplify sequences encoding the human growth hormone, erythropoietin and  
CC IFN-alpha2 proteins, and signal sequences used to control their  
CC secretion, and change these sequences in order to alter their efficacy.  
CC One example of modifications is the addition of polyethylene glycol  
CC moieties. The proteins could then be produced in cell cultures and  
CC isolated for use in the treatment of disorders such as those associated  
CC with growth hormone, erythropoietin or IFN-alpha2.  
XX  
SQ Sequence 32 BP; 7 A; 13 C; 6 G; 6 T; 0 other;

Query Match 61.0%; Score 12.2; DB 21; Length 32;  
Best Local Similarity 82.4%; Pred. No. 2.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tgggttcgaatcgacc 20  
||| ||| ||| ||| |||  
Db 21 TGGATTCTAATCGGATC 5

RESULT 15  
AAA74783/c  
ID AAA74783 standard; DNA; 34 BP.  
XX  
AC AAA74783;  
XX  
DT 17-JAN-2001 (first entry)  
XX  
DE Human growth hormone mutagenic primer BB33.  
XX  
XX Erythropoietin; growth hormone; IFN-alpha2; free cysteine residue;  
KW PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200042175-A1.  
PN  
XX 20-JUL-2000.  
PD  
XX 14-JAN-2000; 2000WO-US00931.  
PF  
XX 14-JAN-1999; 99US-0116041.  
PR  
XX (BOLD-) BOLDER BIOTECHNOLOGY INC.  
PA  
XX Cox GN, Doherty DH, Rosendahl MS;  
PI  
XX WPI; 2000-476056/41.  
DR  
XX Producing a soluble protein having a free cysteine comprises exposing a  
PT host cell expressing the soluble protein to a cysteine blocking agent,  
PT useful for producing recombinant human growth factor and erythropoietin  
PT .

PT  
XX  
PS  
XX  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
XX  
SQ

Example 4; Page 24; 86pp; English.

The present invention concerns novel methods of producing proteins with free cysteine residues. The PCR primers AAA74770-A74854 were used to amplify sequences encoding the human growth hormone, erythropoietin and IFN-alpha2 proteins, and signal sequences used to control their secretion, and change these sequences in order to alter their efficacy. One example of modifications is the addition of polyethylene glycol moieties. The proteins could then be produced in cell cultures and isolated for use in the treatment of disorders such as those associated with growth hormone, erythropoietin or IFN-alpha2.

Sequence 34 BP; 8 A; 11 C; 9 G; 6 T; 0 other;

Query Match 61.08; Score 12.2; DB 21; Length 34;  
Best Local Similarity 82.4%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 tggtttccaatcgacc 20  
||| ||| ||||| |  
Db 29 TGGATTCTATCGGATC 13

Search completed: October 2, 2001, 16:18:43  
Job time: 15487 sec

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:49 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-12

Perfect score: 20

Sequence: 1 cctgacatcagtagcatctc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-12
2	15	75.0	15	3	US-09-377-310-32
c 3	13.8	69.0	17	1	US-08-373-124A-1431
c 4	13.8	69.0	17	1	US-08-435-628-1431
c 5	13.8	69.0	30	1	US-08-235-503B-64
c 6	13.8	69.0	30	5	PCT-US95-05265-64
c 7	13.6	68.0	42	1	US-07-834-539A-12
c 8	13.6	68.0	42	1	US-08-053-131-64
c 9	13.6	68.0	42	1	US-08-645-641-64
c 10	13.6	68.0	42	1	US-07-853-408B-64
c 11	13.6	68.0	42	1	US-08-096-762-64
c 12	13.6	68.0	42	2	US-08-800-353-12
c 13	13.6	68.0	42	2	US-08-308-865-64
c 14	13.6	68.0	42	4	US-09-042-353-188
c 15	13.6	68.0	42	4	US-09-042-353-225
c 16	13.6	68.0	42	5	PCT-US92-06185-12
c 17	13.6	68.0	42	5	PCT-US92-10993-64
c 18	13.2	66.0	30	1	US-07-832-905B-17
c 19	13.2	66.0	30	2	US-08-700-757-17
c 20	13	65.0	23	1	US-08-464-531-59
c 21	13	65.0	23	2	US-08-461-598-59
c 22	13	65.0	23	3	US-08-322-137-59
c 23	13	65.0	36	2	US-08-585-684B-937
c 24	13	65.0	36	4	US-09-038-073-937
c 25	12.8	64.0	21	1	US-08-368-803-20
c 26	12.8	64.0	21	2	US-08-578-096A-21
c 27	12.8	64.0	21	3	US-08-790-517-11

28	12.8	64.0	21	3	US-09-240-426-21	Sequence 21, Appl
29	12.8	64.0	21	3	US-09-219-932-17	Sequence 17, Appl
c 30	12.8	64.0	27	1	US-08-243-542-20	Sequence 20, Appl
c 31	12.8	64.0	27	1	US-08-477-407-20	Sequence 20, Appl
c 32	12.8	64.0	27	1	US-08-484-355-20	Sequence 20, Appl
c 33	12.4	62.0	18	1	US-08-373-124A-2219	Sequence 2219, Ap
c 34	12.4	62.0	18	1	US-08-435-628-2219	Sequence 2219, Ap
c 35	12.4	62.0	38	1	US-08-373-124A-2004	Sequence 2004, Ap
c 36	12.4	62.0	38	1	US-08-435-628-2004	Sequence 2004, Ap
c 37	12.4	62.0	38	2	US-08-292-620A-2091	Sequence 2091, Ap
c 38	12.4	62.0	38	3	US-09-071-845-2091	Sequence 2091, Ap
c 39	12.4	62.0	41	1	US-08-231-342-9	Sequence 9, Appl
c 40	12.4	62.0	50	4	US-08-628-747-24	Sequence 24, Appl
c 41	12.2	61.0	28	2	US-07-814-220-20	Sequence 20, Appl
c 42	12.2	61.0	28	2	US-07-812-421-20	Sequence 20, Appl
c 43	12.2	61.0	29	2	US-07-814-220-19	Sequence 19, Appl
c 44	12.2	61.0	29	2	US-07-812-421-19	Sequence 19, Appl
c 45	12.2	61.0	31	2	US-08-859-998-1327	Sequence 1327, Ap

ALIGNMENTS

RESULT 1  
US-09-377-310-12  
; Sequence 12, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-12

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20  
Db 1 cctgacatcagtagcatctc 20

RESULT 2  
US-09-377-310-32  
; Sequence 32, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-32

Query Match 75.0%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgacatcagtagcat 17  
DB 1 tgacatcagtagcat 15

## RESULT 3

US-08-373-124A-1431/c  
; Sequence 1431, Application US/08373124A  
; Patent No. 5646042

; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/373,124A  
; FILING DATE: January 13, 1995

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994

; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992

; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992

; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/035  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 1431:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-373-124A-1431

Query Match 69.0%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 79;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gacatcagtagcatctc 20  
DB 17 GACATCAGGAGCAACTC 1

## RESULT 4

US-08-435-628-1431/c  
; Sequence 1431, Application US/08435628  
; Patent No. 5817796

; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,628  
; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,124  
; FILING DATE: January 13, 1995

; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994

; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992

; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/035  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 1431:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-435-628-1431

Query Match 69.0%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 79;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gacatcagtagcatctc 20  
DB 17 GACATCAGGAGCAACTC 1

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RESULT 5
PCT-US95-503B-64/c
; Sequence 64, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Balchwal, Vijay R
; APPLICANT: Strulovici, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,503B
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-503B-64

Query Match 69.0%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcat 17
Db 27 CCTGATATCATTAGCAT 11

RESULT 6
PCT-US95-05265-64/c
; Sequence 64, Application PC/TUS9505265
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,503
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-05265-64

Query Match 69.0%; Score 13.8; DB 5; Length 30;
Best Local Similarity 88.2%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcat 17
Db 27 CCTGATATCATTAGCAT 11

RESULT 7
US-07-834-539A-12/c
; Sequence 12, Application US/07834539A
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,539A
; FILING DATE: 1992-02-05
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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US-07-834-539A-12

Query Match 68.0%; Score 13.6; DB 1; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| |  
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 8

US-08-053-131-64/c  
; Sequence 64, Application US/08053131  
; Patent No. 5661016  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,131  
; FILING DATE: 26-APR-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860  
; FILING DATE: 16-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/810,279  
; FILING DATE: 17-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,408  
; FILING DATE: 18-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-9-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 42 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (primer)  
; US-08-053-131-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| |  
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 9

US-08-645-641-64/c  
; Sequence 64, Application US/08645641  
; Patent No. 5719032  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 150  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/645,641  
; FILING DATE: 20-MAY-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/904,068  
; FILING DATE: 23-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-000913  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 42 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (primer)  
; US-08-645-641-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| |  
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 10

US-07-853-408B-64/c  
; Sequence 64, Application US/07853408B  
; Patent No. 5789650  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 150  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 19920318  
APPLICATION NUMBER: US/07/853,408B  
REFERENCE/DOCKET NUMBER: 14643-9  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (primer)  
US-07-853-408B-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| I  
DB 35 CCAGACATCAAAAGCATCAC 16

## RESULT 11

US-08-096-762-64/c  
Sequence 64, Application us/08096762  
Patent No. 5814318  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 210  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,762  
FILING DATE: 22-JUL-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-4  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (primer)  
US-08-096-762-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| I  
DB 35 CCAGACATCAAAAGCATCAC 16

## RESULT 12

US-08-800-353-12/c  
Sequence 12, Application US/08800353  
Patent No. 5874299  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,353  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/834,539  
FILING DATE: 1992-02-05  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-5  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-800-353-12

Query Match 68.0%; Score 13.6; DB 2; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| |  
Db 35 CCAGACATCAAAAGCATCAC 16

## RESULT 13

US-08-308-865-64/c  
; Sequence 64, Application US/08308865  
; Patent No. 5877397  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 150  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/308,865  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/145,707  
; FILING DATE:  
; APPLICATION NUMBER: US/07/904,068  
; FILING DATE: 23-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-9-1-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 42 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (primer)  
; US-08-308-865-64

Query Match 68.0%; Score 13.6; DB 2; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| |  
Db 35 CCAGACATCAAAAGCATCAC 16

## RESULT 14

US-09-042-353-188/c  
; Sequence 188, Application US/09042353  
; Patent No. 6255458  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils

; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 421  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,353  
; FILING DATE: 13-MAR-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/810,279  
; FILING DATE: 17-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/853,408  
; FILING DATE: 18-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/904,068  
; FILING DATE: 23-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/990,860  
; FILING DATE: 16-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,131  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/096,762  
; FILING DATE: 22-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/155,301  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/161,739  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/165,699  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/209,741  
; FILING DATE: 09-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/352,322  
; FILING DATE: 07-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/544,404  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/728,463  
; FILING DATE: 10-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US96/16433  
; FILING DATE: 10-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/758,417  
; FILING DATE: 02-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/21803  
; FILING DATE: 01-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 014643-009040US  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-042-353-188

Query Match 68.0%; Score 13.6; DB 4; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| I  
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 15  
US-09-042-353-225/C  
Sequence 225, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699

FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/16433  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/21803  
FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 225:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-042-353-225

Query Match 68.0%; Score 13.6; DB 4; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20  
|| ||||| ||||| I  
Db 35 CCAGACATCAAAAGCATCAC 16

Search completed: October 2, 2001, 16:03:50  
Job time: 14594 sec



MOLECULE TYPE: DNA (genomic)  
US-08-466-588-52

Query Match 76.0%; Score 15.2; DB 8; Length 40;  
Best Local Similarity 85.0%; Pred. No. 6.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 attctcgcgtcgtgtaa 20  
|||||  
DB 21 ATTCTCGGTGTCGCCGAA 2

## RESULT 5

PCT-US00-18999-37  
; Sequence 37, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-37

Query Match 75.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tctcgcgtcgtggtg 17  
|||||  
DB 1 tctcgcgtcgtggtg 15

## RESULT 6

US-09-377-310-37  
; Sequence 37, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-37

Query Match 75.0%; Score 15; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tctcgcgtcgtggtg 17  
|||||  
DB 1 tctcgcgtcgtggtg 15

## RESULT 7

US-09-757-100B-37  
; Sequence 37, Application US/09757100B  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-37

Query Match 75.0%; Score 15; DB 29; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tctcgcgtcgtggtg 17  
|||||  
DB 1 tctcgcgtcgtggtg 15

## RESULT 8

US-09-144-428-31  
; Sequence 31, Application US/09144428  
; GENERAL INFORMATION:  
; APPLICANT: BAYER CORPORATION, The  
; APPLICANT: TAMBURINI, Paul P  
; APPLICANT: DAVIS, Gary  
; APPLICANT: DELARIA, Katherine A  
; APPLICANT: MARLOR, Christopher W  
; APPLICANT: MULLER, Daniel K  
; TITLE OF INVENTION: HUMAN BIKUNIN  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 S. Wacker Drive Suite 3200  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/144,428  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/03894  
; FILING DATE: 10-MAR-1997

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,106  
FILING DATE: 11-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,793  
FILING DATE: 14-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/725,251  
FILING DATE: 04-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAO, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 96,223-II  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 913-0001  
TELEFAX: (312) 913-0002  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-09-144-428-31

Query Match 74.0%; Score 14.8; DB 15; Length 35;  
Best Local Similarity 88.9%; Pred. No. 9.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgga 20  
||||| ||||| |||||  
Db 6 TCCTCACTGCTGCGGAA 23

## RESULT 9

US-09-218-913B-31  
Sequence 31, Application US/09218913B  
GENERAL INFORMATION:  
APPLICANT: Hall, Roderick L.  
APPLICANT: Poll, Christopher T.  
APPLICANT: Newton, Benjamin B.  
APPLICANT: Taylor, William J.A.  
TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance  
FILE REFERENCE: 98,736  
CURRENT APPLICATION NUMBER: US/09/218,913B  
CURRENT FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 31  
LENGTH: 35  
TYPE: DNA  
ORGANISM: S. cerevisiae  
US-09-218-913B-31

Query Match 74.0%; Score 14.8; DB 16; Length 35;  
Best Local Similarity 88.9%; Pred. No. 9.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgga 20  
||||| ||||| |||||  
Db 6 tctctactgctgctgga 23

## RESULT 10

US-09-441-966-31  
Sequence 31, Application US/09441966  
GENERAL INFORMATION:  
APPLICANT: Hall, Roderick L.  
APPLICANT: Poll, Christopher T.  
APPLICANT: Newton, Benjamin B.

APPLICANT: Taylor, William J.A.  
TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance  
FILE REFERENCE: 98,736-A  
CURRENT APPLICATION NUMBER: US/09/441,966  
CURRENT FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 09/218,913  
PRIOR FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 31  
LENGTH: 35  
TYPE: DNA  
ORGANISM: S. cerevisiae  
US-09-441-966-31

Query Match 74.0%; Score 14.8; DB 18; Length 35;  
Best Local Similarity 88.9%; Pred. No. 9.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgga 20  
||||| ||||| |||||  
Db 6 tctctactgctgctgga 23

## RESULT 11

US-08-472-801-1314  
Sequence 1314, Application US/08472801  
GENERAL INFORMATION:  
APPLICANT: Heses 2  
APPLICANT: Smith, Larry J.  
TITLE OF INVENTION: Method and Compositions for Cellular  
FILE REFERENCE: Heses 2  
CURRENT APPLICATION NUMBER: US/08/472,801  
CURRENT FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 3601  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1314  
LENGTH: 37  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-472-801-1314

Query Match 72.0%; Score 14.4; DB 8; Length 37;  
Best Local Similarity 93.8%; Pred. No. 1.4e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgg 18  
||||| ||||| |||||  
Db 5 tctctgctgctgctgg 20

## RESULT 12

US-08-668-235-1314  
Sequence 1314, Application US/08668235  
GENERAL INFORMATION:  
APPLICANT: Larry J. Smith  
TITLE OF INVENTION: Methods and Compositions for Cellular  
FILE REFERENCE: Heses-1  
CURRENT APPLICATION NUMBER: US/08/668,235  
CURRENT FILING DATE: 1996-06-17  
EARLIER APPLICATION NUMBER: 07/748,997  
EARLIER FILING DATE: 08/23/91  
EARLIER APPLICATION NUMBER: 08/426,781  
EARLIER FILING DATE: 04/22/95  
EARLIER APPLICATION NUMBER: 08/472,801  
EARLIER FILING DATE: 06/07/95  
NUMBER OF SEQ ID NOS: 3629  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1314

```

; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-1314

```

Query Match 72.0%; Score 14.4; DB 10;  
Best Local Similarity 93.8%; Pred. No. 1.4e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels

**Qy**      3 tctcgcgctgctgg 18  
          |||||  
**Dd**      5 tctcgcgctgctgctgg 20

RESULT 13

PCT-US97-06104-16/c  
; Sequence 16, Application PC/TUS9706104

```

; GENERAL INFORMATION:
; APPLICANT: University of Massachusetts
; TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-BARR
; VIRUS ACTIVITY
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

```

Query Match 71.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.7e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 2 ttctctgctgctggtgga 20  
|| ||||| ||||| |||||  
Db 20 TTGCTCGCAGCTGGAGGA 2

**RESULT** 14

US-60-232-638-132115  
; Sequence 132115, Application US/60232638  
; GENERAL INFORMATION:

```

; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132115
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces Cerevisae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YPL144W
; US-60-232-638-132115

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Query Match	68.0%;	Score 13.6;	DB 55;	Length 25;
Best Local Similarity	80.0%;	Pred. No. 3.3e+04;		
Matches 16:	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

Qy 1 attcctcgtcgtggtgga 20  
|||  
Db 6 atccgtcgtactggttcaa 25

RESULT 15

```

US-60-234-017-326383/c
; Sequence 326383, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326383
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA153229
US-60-234-017-326383

```

Query Match 68.0%; Score 13.6; DB 55; Length 25;  
Best Local Similarity 80.0%; Pred. NO. 3.3e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 attcctcgtcgtggtgga 20  
||||| ||||| || ||||| ||  
Db 22 ATCCACGCTACTCGTGCAA 3

Search completed: October 2, 2001, 21:50:18  
Job time: 24531 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:05 ; Search time 2173.58 Seconds  
(without alignments)  
19.290 Million cell updates/sec

Title: US-09-757-100B-17

Perfect score: 20

Sequence: 1 attctcgtctgctggaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	14	70.0	18	6	US-09-477-962-58
c 2	13.4	67.0	20	6	US-09-766-450-39
c 3	13.4	67.0	20	6	US-09-198-452A-5835
c 4	13.4	67.0	44	8	US-60-253-456-27973
c 5	13	65.0	31	6	US-09-801-274-757
c 6	12.8	64.0	17	5	US-09-371-772B-6946
c 7	12.8	64.0	17	5	US-09-708-690-6946
c 8	12.8	64.0	17	5	US-09-708-690-9123
c 9	12.8	64.0	47	8	US-60-252-833-5936
c 10	12.6	63.0	20	6	US-09-198-452A-6492
c 11	12.6	63.0	24	7	US-09-912-935-48
c 12	12.4	62.0	31	6	US-09-801-274-638
c 13	12.4	62.0	38	6	US-09-546-745A-4473
c 14	12.4	62.0	38	8	US-60-278-232-3939
c 15	12.4	62.0	48	7	US-09-864-785-3115
c 16	12.2	61.0	31	5	US-09-574-376B-160
c 17	12	60.0	16	5	US-09-371-772B-5835
c 18	12	60.0	16	5	US-09-708-690-5835
c 19	12	60.0	17	5	US-09-371-772B-4795
c 20	12	60.0	17	5	US-09-371-772B-4796
c 21	12	60.0	17	5	US-09-371-772B-4797
c 22	12	60.0	17	5	US-09-371-772B-6943
c 23	12	60.0	17	5	US-09-371-772B-6944
c 24	12	60.0	17	5	US-09-371-772B-6945
c 25	12	60.0	17	5	US-09-708-690-4795

c 26	12	60.0	17	5	US-09-708-690-4796	Sequence 4796, Ap
c 27	12	60.0	17	5	US-09-708-690-4797	Sequence 4797, Ap
c 28	12	60.0	17	5	US-09-708-690-6943	Sequence 6943, Ap
c 29	12	60.0	17	5	US-09-708-690-6944	Sequence 6944, Ap
c 30	12	60.0	17	5	US-09-708-690-6945	Sequence 6945, Ap
c 31	12	60.0	17	5	US-09-708-690-7664	Sequence 7664, Ap
c 32	12	60.0	17	5	US-09-708-690-7665	Sequence 7665, Ap
c 33	11.8	59.0	18	7	US-09-787-252-44	Sequence 44, Appl
c 34	11.8	59.0	20	6	US-09-198-452A-6820	Sequence 6820, Ap
c 35	11.8	59.0	48	5	US-09-532-537B-2863	Sequence 2863, Ap
c 36	11.8	59.0	48	7	US-09-864-785-3510	Sequence 3510, Ap
c 37	11.6	58.0	20	6	US-09-198-452A-4453	Sequence 4453, Ap
c 38	11.6	58.0	38	6	US-09-535-373-54	Sequence 54, Appl
c 39	11.6	58.0	48	6	US-09-509-098-71	Sequence 71, Appl
c 40	11.4	57.0	21	6	US-09-508-891-16	Sequence 16, Appl
c 41	11.4	57.0	22	5	US-09-931-700-11	Sequence 11, Appl
c 42	11.4	57.0	25	5	US-09-628-313-84	Sequence 84, Appl
c 43	11.4	57.0	27	5	US-09-622-646-9	Sequence 9, Appl
c 44	11.4	57.0	31	6	US-09-801-274-122	Sequence 122, App
c 45	11.4	57.0	31	6	US-09-801-274-1390	Sequence 1390, Ap

ALIGNMENTS

RESULT 1

US-09-477-962-58/c  
; Sequence 58, Application US/09477962  
; GENERAL INFORMATION:

; APPLICANT: SHEN, BEN  
; APPLICANT: DU, LIANGCHENG  
; APPLICANT: SANCHEZ, CESAR  
; APPLICANT: CHEN, MEI  
; APPLICANT: EDWARDS, DANIEL J.  
; TITLE OF INVENTION: BLEOMYCIN GENE CLUSTER COMPONENTS AND THEIR USES  
; FILE REFERENCE: 407T-895820US  
; CURRENT APPLICATION NUMBER: US/09/477,962  
; CURRENT FILING DATE: 2000-01-05  
; PRIOR APPLICATION NUMBER: 60/115,435  
; PRIOR FILING DATE: 1999-01-06  
; PRIOR APPLICATION NUMBER: 60/118,848  
; PRIOR FILING DATE: 1999-02-05  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 58  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-477-962-58

Query Match 70.0%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cctcgtctgctggtg 17

Db 17 CCTCGTCTGCTGTG 4

RESULT 2

US-09-766-450-39/c  
; Sequence 39, Application US/09766450  
; GENERAL INFORMATION:

; APPLICANT: COLLINS, COLIN  
; APPLICANT: VOLIK, STANISLAV  
; APPLICANT: GRAY, JOE W.  
; APPLICANT: ALBERTSON, DONNA G.  
; APPLICANT: PINKEL, DANIEL  
; TITLE OF INVENTION: Repeat-Free Probes for Molecular

Query Match	67.0%;	Score 13.4;	DB 8;	Length 44;
Best Local Similarity	93.3%;	Pred. No. 4e+03;		

DB 8; Length 44;  
-03;

```

Query Match          64.0%; Score 12.8; DB 5; Length 17;
Best Local Similarity 87.5%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 ctgcgtcgtggtgga 20
        || |||||

```

Db 17 CTTCTGCTGCTGGAA 2

RESULT 7  
US-09-708-690-6946/c  
; Sequence 6946, Application US/09708690  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MEHB00,876-L (400/002)  
; CURRENT APPLICATION NUMBER: US/09/708,690  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6946  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-708-690-6946

Query Match 64.0%; Score 12.8; DB 5; Length 17;  
Best Local Similarity 87.5%; Pred. No. 7e+03; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2;  
Qy 5 ctgcgtcgtcgtgga 20  
||| ||||| |||||  
Db 17 CTTCTGCTGCTGGAA 2

RESULT 8  
US-09-708-690-9123/c  
; Sequence 9123, Application US/09708690  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MEHB00,876-L (400/002)  
; CURRENT APPLICATION NUMBER: US/09/708,690  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9123  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-708-690-9123

Query Match 64.0%; Score 12.8; DB 5; Length 17;  
Best Local Similarity 87.5%; Pred. No. 7e+03; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2;  
Qy 5 ctgcgtcgtcgtgga 20  
||| ||||| |||||  
Db 16 CTTCTGCTGCTGGAA 1

RESULT 9  
US-60-252-833-5936/c  
; Sequence 5936, Application US/60252833  
; GENERAL INFORMATION:  
; APPLICANT: Glenn, Matthew  
; APPLICANT: Grigor, Murray R  
; TITLE OF INVENTION: Compositions isolated from bovine  
; TITLE OF INVENTION: tissues and methods for their use.  
; FILE REFERENCE: 1052P2  
; CURRENT APPLICATION NUMBER: US/60/252,833  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 43535  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5936  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Bovine  
US-60-252-833-5936

Query Match 64.0%; Score 12.8; DB 8; Length 47;  
Best Local Similarity 87.5%; Pred. No. 7.8e+03; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2;  
Qy 2 ttctcgtcgtcgtggtg 17  
||| ||||| |||||  
Db 27 TTCATCGCTGCTGCTG 12

RESULT 10  
US-09-198-452A-6492  
; Sequence 6492, Application US/09198452A  
; GENERAL INFORMATION:  
; APPLICANT: Griflais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 6492  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-6492

Query Match 63.0%; Score 12.6; DB 6; Length 20;  
Best Local Similarity 78.9%; Pred. No. 8.9e+03; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 4;  
Qy 1 attctcgtcgtcgtgga 19  
| ||||| ||||| ||  
Db 2 agtctcgtcgtgataga 20

RESULT 11  
US-09-912-935-48/c  
; Sequence 48, Application US/09912935  
; GENERAL INFORMATION:

; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: primer H2728F  
US-09-912-935-48

Query Match 63.0%; Score 12.6; DB 7; Length 24;  
Best Local Similarity 78.9%; Pred. No. 9.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ttctcgtcgtcgttgaa 20  
||| ||||| ||| |||||  
Db 21 TTTCTCGACGCCGAGGAA 3

RESULT 12  
US-09-801-274-638  
; Sequence 638, Application US/09801274  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; CURRENT APPLICATION NUMBER: US/09/801,274  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US 60/187,510  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: US 60/206,129  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 1802  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 638  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-801-274-638

Query Match 62.0%; Score 12.4; DB 6; Length 31;  
Best Local Similarity 81.2%; Pred. No. 1.2e+04;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ctccgtcgtcgttgaa 20  
||| ||||| ||| |||||  
Db 5 ctccctcgtcgttgaa 20

RESULT 13  
US-09-546-745A-4473  
; Sequence 4473, Application US/09546745A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: Zwick, Michael  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules  
; FILE REFERENCE: 237/193  
; CURRENT APPLICATION NUMBER: US/09/546,745A  
; CURRENT FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 7043

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4473  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; NAME/KEY: misc\_feature  
; LOCATION: (17)..(26)  
; OTHER INFORMATION: positions 17-26 n stands for any nucleotide, positions 19-26 n  
; OTHER INFORMATION: be optionally absent  
US-09-546-745A-4473

Query Match 62.0%; Score 12.4; DB 6; Length 38;  
Best Local Similarity 64.3%; Pred. No. 1.2e+04;  
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 cctcgtcgtcgtg 17  
||| ||||| ||| |||||  
Db 1 ccucgucgucgaug 14

RESULT 14  
US-60-278-232-3939  
; Sequence 3939, Application US/60278232  
; GENERAL INFORMATION:  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Lal, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide  
; FILE REFERENCE: GX-0011 P  
; CURRENT APPLICATION NUMBER: US/60/278,232  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 12,557  
; SOFTWARE: PERL Program  
; SEQ ID NO 3939  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: SNP00049413  
; NAME/KEY: snp  
; LOCATION: 26  
; OTHER INFORMATION: 229881.1, 569, T->C  
US-60-278-232-3939

Query Match 62.0%; Score 12.4; DB 8; Length 38;  
Best Local Similarity 92.9%; Pred. No. 1.2e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 attcctcgtcgtg 14  
||| ||||| |||||  
Db 23 attcctcgtcgtg 36

RESULT 15  
US-09-864-785-3115  
; Sequence 3115, Application US/09864785  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBH800-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23

```
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3115
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-3115

Query Match      62.0%; Score 12.4; DB 7; Length 48;
Best Local Similarity 78.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 cgctgctggtgga 20
Db 2 cgcugcugaggaa 15

Search completed: October 2, 2001, 16:55:05
Job time: 17668 sec
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:04 ; Search time 2173.58 Seconds  
(without alignments)  
19.290 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggaggagctcagtggtg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	13.2	66.0	18	5	US-09-650-012A-1062
c 2	12.6	63.0	26	7	US-09-922-146-6
c 3	12.6	63.0	32	6	US-09-545-777-8
c 4	12.2	61.0	31	6	US-09-817-879-5909
c 5	12	60.0	37	5	US-09-708-690-18238
c 6	12	60.0	38	5	US-09-942-325-6
c 7	11.8	59.0	22	6	US-09-883-152-59
c 8	11.8	59.0	31	5	US-09-574-376B-1160
c 9	11.8	59.0	31	5	US-09-574-376B-1320
c 10	11.8	59.0	39	5	US-09-771-372-9
c 11	11.6	58.0	31	1	PCT-US01-19353-77
c 12	11.6	58.0	31	7	US-09-786-033-19
c 13	11.6	58.0	39	7	US-09-514-673-26
c 14	11.6	58.0	40	7	US-09-563-794-69
c 15	11.4	57.0	30	5	US-09-310-735A-140
c 16	11.4	57.0	30	5	US-09-310-735A-151
c 17	11.4	57.0	30	5	US-09-310-844B-140
c 18	11.4	57.0	30	5	US-09-310-844B-151
c 19	11.2	56.0	17	7	US-09-818-875-1934
c 20	11.2	56.0	17	7	US-09-818-875-1935
c 21	11.2	56.0	20	6	US-09-421-971-19
c 22	11.2	56.0	20	6	US-09-527-376-6
c 23	11.2	56.0	20	7	US-09-906-158-111
c 24	11.2	56.0	21	6	US-09-765-081-81
c 25	11.2	56.0	22	5	US-09-941-992-470

ALIGNMENTS

RESULT 1

US-09-650-012A-1062/c  
; Sequence 1062, Application US/09650012A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Re  
; TITLE OF INVENTION: Immune Responses  
; FILE REFERENCE: 250/130 (MBHB00-900-A)  
; CURRENT APPLICATION NUMBER: US/09/650,012A  
; CURRENT FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 08/585,684  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: US 60/000,951  
; PRIOR FILING DATE: 1995-07-07  
; PRIOR APPLICATION NUMBER: US 09/038,073  
; PRIOR FILING DATE: 1998-03-11  
; NUMBER OF SEQ ID NOS: 2285  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1062  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-650-012A-1062

Query Match 66.0%; Score 13.2; DB 5; Length 18;  
Best Local Similarity 83.3%; Pred. No. 5.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtggt 18

Db 18 CTGGGGGAGGCTGAGGTT 1

RESULT 2

US-09-922-146-6/c  
; Sequence 6, Application US/09922146  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowsett  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION  
; FILE REFERENCE: RPS-0252  
; CURRENT APPLICATION NUMBER: US/09/922,146  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 48

; SEQ ID NO 6  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Probe  
US-09-922-146-6

Query Match 63.0%; Score 12.6; DB 7; Length 26;  
Best Local Similarity 78.9%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 tagggaggctcagtggtg 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 TAGCGGATCCCGAGTTGG 1

RESULT 3  
US-09-545-777-8/c  
; Sequence 8, Application US/09545777  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Hua  
; APPLICANT: Jarnigan, Kurt  
; APPLICANT: Zhou, Hua  
; APPLICANT: Greene L., Amy  
; APPLICANT: Thode, Silke  
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID AND PARALLEL  
; TITLE OF INVENTION: ASSAY DEVELOPMENT, FOR CHARACTERIZATION OF THE  
; TITLE OF INVENTION: ACTIVITIES OF BIOLOGICAL RESPONSE MODIFIERS  
; FILE REFERENCE: 5050-0015  
; CURRENT APPLICATION NUMBER: US/09/545,777  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/128,631  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer TK3  
US-09-545-777-8

Query Match 63.0%; Score 12.6; DB 6; Length 32;  
Best Local Similarity 78.9%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 tagggaggctcagtggtg 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 26 TGGGGGAGGCTAACTAGG 8

RESULT 4  
US-09-817-879-5909/c  
; Sequence 5909, Application US/09817879  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBHB00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5909  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature

; LOCATION:  
; OTHER INFORMATION: DNazyme  
US-09-817-879-5909

Query Match 61.0%; Score 12.2; DB 6; Length 31;  
Best Local Similarity 82.4%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 ggggaggctcagtggtg 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 31 GGGGAGGCTCGTGTGTAG 15

RESULT 5  
US-09-708-690-18238  
; Sequence 18238, Application US/09708690  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00,876-L (400/002)  
; CURRENT APPLICATION NUMBER: US/09/708,690  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18238  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-708-690-18238

Query Match 60.0%; Score 12; DB 5; Length 37;  
Best Local Similarity 60.0%; Pred. No. 2.2e+04;  
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 ctaggggaggctcagtggtg 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 18 cqagugaggucacuguggg 37

RESULT 6  
US-09-942-325-6/c  
; Sequence 6, Application US/09942325  
; GENERAL INFORMATION:  
; APPLICANT: Iacovitti, Lorraine  
; APPLICANT: Kessler, Mark  
; TITLE OF INVENTION: The Human Tyrosine Hydroxylase Promoter  
; TITLE OF INVENTION: Sequence and Related Methods and Compositions  
; FILE REFERENCE: IAC01-NP001  
; CURRENT APPLICATION NUMBER: US/09/942,325  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 60/228931  
; PRIOR FILING DATE: 2000-02-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 38



; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-942-325-6

Query Match 60.0%; Score 12; DB 5; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ggctcagtg 20  
|||||  
Db 34 GGCTCAGTGG 23

## RESULT 7

US-09-883-152-59  
; Sequence 59, Application US/09883152  
; GENERAL INFORMATION:  
; APPLICANT: Kennedy, Giulia  
; APPLICANT: Kang, Sanmao  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne Bennett  
; TITLE OF INVENTION: POLYNUCLEOTIDES RELATED TO COLON CANCER  
; FILE REFERENCE: 2300-1663  
; CURRENT APPLICATION NUMBER: US/09/883,152  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/211,835  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-883-152-59

Query Match 59.0%; Score 11.8; DB 6; Length 22;  
Best Local Similarity 86.7%; Pred. No. 2.7e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 aggggaggtcagtg 17  
|||||  
Db 8 aggggaggtcagtg 22

## RESULT 8

US-09-574-376B-1160  
; Sequence 1160, Application US/09574376B  
; GENERAL INFORMATION:  
; APPLICANT: Warrington, Janet  
; APPLICANT: Shah, Nila  
; APPLICANT: Gingeras, Thomas Raymond  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms  
; FILE REFERENCE: 3229.2  
; CURRENT APPLICATION NUMBER: US/09/574,376B  
; CURRENT FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 1330  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1160  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
US-09-574-376B-1160

Query Match 59.0%; Score 11.8; DB 5; Length 31;  
Best Local Similarity 76.5%; Pred. No. 2.7e+04;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ctaggggaggtcagtg 17  
|||||  
Db 14 ctmggggtcggtcagtg 30

## RESULT 9

US-09-574-376B-1320  
; Sequence 1320, Application US/09574376B  
; GENERAL INFORMATION:  
; APPLICANT: Warrington, Janet  
; APPLICANT: Shah, Nila  
; APPLICANT: Gingeras, Thomas Raymond  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms  
; FILE REFERENCE: 3229.2  
; CURRENT APPLICATION NUMBER: US/09/574,376B  
; CURRENT FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 1330  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1320  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
US-09-574-376B-1320

Query Match 59.0%; Score 11.8; DB 5; Length 31;  
Best Local Similarity 76.5%; Pred. No. 2.7e+04;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 ggggaggtcagtg 20  
|||||  
Db 6 ggtggtcggtcagtg 22

## RESULT 10

US-09-771-372-9  
; Sequence 9, Application US/09771372  
; GENERAL INFORMATION:  
; APPLICANT: LOEHRLEIN, CHRISTINE  
; APPLICANT: POLLART, DAN  
; APPLICANT: SHALER, THOMAS  
; APPLICANT: STEPHENS, KATHY  
; APPLICANT: TAN, YUPING  
; APPLICANT: WONG, LINDA  
; APPLICANT: MONFORTE, JOSEPH  
; TITLE OF INVENTION: METHODS FOR ANALYSIS OF GENE EXPRESSION  
; FILE REFERENCE: 14-004510US  
; CURRENT APPLICATION NUMBER: US/09/771,372  
; CURRENT FILING DATE: 2001-01-27  
; PRIOR APPLICATION NUMBER: 60/179,006  
; PRIOR FILING DATE: 2000-01-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-771-372-9

Query Match 59.0%; Score 11.8; DB 5; Length 39;  
Best Local Similarity 86.7%; Pred. No. 2.7e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ggggaggtcagtg 19  
|||||  
Db 16 ggggaggtcagtg 30

```
RESULT 11
; Sequence 77, Application PC/TUS0119353
; GENERAL INFORMATION:
; APPLICANT: Anthony, James
; APPLICANT: Lorincz, Attila
; APPLICANT: Williams, Inna
; APPLICANT: Troy, John
; APPLICANT: Tang, Yanlin
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS BY TYPE-SPECIFIC HYBRID
; FILE REFERENCE: 2629-4017PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19353
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/594,839
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DP-1
; OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
; OTHER INFORMATION: probe
PCT-US01-19353-77

Query Match      58.0%; Score 11.6; DB 1; Length 31;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
   |||| ||||| ||||
Db 5 taggtgaggtcagtg 22

RESULT 12
US-09-786-033-19
; Sequence 19, Application US/09786033
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark Henry
; APPLICANT: Weiss, Jurgen
; TITLE OF INVENTION: METHODS FOR IMPROVING THE FUNCTION OF HETEROLOGOUS G
; FILE REFERENCE: 01142.102-00304
; CURRENT APPLICATION NUMBER: US/09/786,033
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-786-033-19

Query Match      58.0%; Score 11.6; DB 7; Length 31;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
   || | ||||| ||||
Db 12 tacagatggctcagtg 29

RESULT 13
US-09-514-673-26/c
```

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; Sequence 26, Application US/09514673
; GENERAL INFORMATION:
; APPLICANT: DOWDY, STEVEN F.
; TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS FOR USING SAME
; FILE REFERENCE: 49054(71742)
; CURRENT APPLICATION NUMBER: US/09/514,673
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/122,757
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: 60/151,291
; PRIOR FILING DATE: 1999-08-29
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-514-673-26
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Query Match      58.0%; Score 11.6; DB 7; Length 39;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
   ||||| ||||| |||
Db 33 TGGGGGAGGCTAACTGAG 16
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RESULT 14
US-09-563-794-69/c
; Sequence 69, Application US/09563794
; GENERAL INFORMATION:
; APPLICANT: Kruger, Martin
; APPLICANT: Welch, Peter J.
; APPLICANT: Barber, Jack R.
; TITLE OF INVENTION: Cellular Regulators of Infectious Agents and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: P-IU 3738
; CURRENT APPLICATION NUMBER: US/09/563,794
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-563-794-69
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Query Match      58.0%; Score 11.6; DB 7; Length 40;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
   ||||| ||||| |||
Db 33 TGGGGGAGGCTAACTGAG 16
```

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RESULT 15
US-09-310-735A-140/G
; Sequence 140, Application US/09310735A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
```

; APPLICANT: Mohan, Venkatraman  
; APPLICANT: Hofstadler, Steven  
; APPLICANT: McNeil, John  
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and  
; FILE REFERENCE: IBIS0015  
; CURRENT APPLICATION NUMBER: US/09/310,735A  
; CURRENT FILING DATE: 1999-05-12  
; PRIOR APPLICATION NUMBER: 09/076,404  
; PRIOR FILING DATE: 1998-05-12  
; NUMBER OF SEQ ID NOS: 393  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 140  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
US-09-310-735A-140

Query Match 57.0%; Score 11.4; DB 5; Length 30;  
Best Local Similarity 92.3%; Pred. No. 4.2e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 aggtctcagtggtg 20  
|| |||||  
Db 14 AGACTCAGTGTGG 2

Search completed: October 2, 2001, 16:55:05  
Job time: 17668 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:16 ; Search time 17695.9 Seconds  
(without alignments)  
16.701 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggaggagctcagtggtgg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 738840595 residues

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	1	PCT-US00-18999-16
2	20	100.0	20	17	US-09-377-310-16
3	20	100.0	20	29	US-09-757-100B-16
4	15	75.0	15	1	PCT-US00-18999-36
5	15	75.0	15	17	US-09-377-310-36
6	15	75.0	15	29	US-09-757-100B-36
7	14.4	72.0	25	26	US-09-660-220-71852
8	14.4	72.0	25	26	US-09-660-220-78149
9	13.8	69.0	25	55	US-60-233-166-385862
10	13.8	69.0	25	55	US-60-233-166-406405
11	13.8	69.0	25	55	US-60-234-017-120917
12	13.8	69.0	25	55	US-60-234-017-120921
13	13.8	69.0	28	1	PCT-US00-26619-18
14	13.6	68.0	25	26	US-09-660-220-94301
15	13.4	67.0	34	7	US-08-305-771A-53
16	13.4	67.0	35	7	US-08-305-771A-57
17	13.2	66.0	18	9	US-08-585-684-2592
18	13.2	66.0	18	9	US-08-585-684A-2592
19	13.2	66.0	20	1	PCT-US99-23205-87
20	13.2	66.0	21	16	US-09-266-682-6
21	13.2	66.0	21	17	US-09-322-134-6
22	13.2	66.0	23	8	US-08-472-801-3446
23	13.2	66.0	23	10	US-08-668-235-3446
24	13.2	66.0	25	55	US-60-233-166-23415
25	13.2	66.0	25	55	US-60-233-166-23416
26	13.2	66.0	25	55	US-60-233-166-3638
27	13.2	66.0	25	55	US-60-234-017-13989
28	13.2	66.0	33	1	PCT-US96-03686B-7
29	13.2	66.0	33	12	US-08-816-772-7
30	13.2	66.0	33	16	US-09-245-024-7
31	13.2	66.0	47	8	US-08-475-228-275
32	13.2	66.0	47	8	US-08-482-080-275
33	13.2	66.0	47	17	US-09-354-947-275
34	13.2	66.0	47	40	US-60-082-614-470
35	13.2	66.0	49	14	US-09-009-490A-94
36	12.8	64.0	25	1	PCT-US00-09865-13
37	12.8	64.0	25	21	US-09-548-933-13
38	12.8	64.0	25	26	US-09-660-220-56881
39	12.8	64.0	25	26	US-09-660-220-56888
40	12.8	64.0	25	26	US-09-660-220-100448
41	12.8	64.0	25	55	US-60-233-166-240151
42	12.8	64.0	25	55	US-60-233-166-364161
43	12.8	64.0	25	55	US-60-233-166-406386
44	12.8	64.0	25	55	US-60-233-166-10838
45	12.8	64.0	25	55	US-60-234-017-309445

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-16  
; Sequence 16, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-16

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtggtg 20  
Db 1 ctaggaggagctcagtggtg 20

RESULT 2  
US-09-377-310-16  
; Sequence 16, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-16

Query Match 100.0%; Score 20; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtggtg 20  
Db 1 ctaggaggagctcagtggtg 20

RESULT 3  
US-09-757-100B-16  
; Sequence 16, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-16

Query Match 100.0%; Score 20; DB 29; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtggtg 20  
Db 1 ctaggaggagctcagtggtg 20

RESULT 4  
PCT-US00-18999-36  
; Sequence 36, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-36

Query Match 75.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 agggaggagctcagtg 17  
Db 1 agggaggagctcagtg 15

RESULT 5  
US-09-377-310-36  
; Sequence 36, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.

```
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-36
```

```
Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 aggggaggtcagtg 17
|||||
Db 1 aggggaggtcagtg 15
```

```
RESULT 6
US-09-757-100B-36
; Sequence 36, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-36
```

```
Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 aggggaggtcagtg 17
|||||
Db 1 aggggaggtcagtg 15
```

```
RESULT 7
US-09-660-220-71852
; Sequence 71852, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
```

```
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71852
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank S76992
US-09-660-220-71852
```

```
Query Match 72.0%; Score 14.4; DB 26; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 aggggaggtcagtg 18
|||||
Db 1 aggggaggtcagtg 16
```

```
RESULT 8
US-09-660-220-78149/c
; Sequence 78149, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78149
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U10439
US-09-660-220-78149
```

```
Query Match 72.0%; Score 14.4; DB 26; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 ggggaggtcagtg 19
|||||
Db 20 GGGGAGACTCAGTG 5
```

```
RESULT 9
US-60-233-166-385862/c
; Sequence 385862, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 385862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccaromyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-60-233-166-385862
```

Query Match 69.0%; Score 13.8; DB 55; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagt 17  
||| ||||| |||||  
Db 22 CTACGGGAGCTCAGT 6

RESULT 10  
US-60-233-166-406405  
; Sequence 406405, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 406405  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta  
US-60-233-166-406405

Query Match 69.0%; Score 13.8; DB 55; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagt 17  
||| ||||| |||||  
Db 6 ctagggaagactcagt 22

RESULT 11  
US-60-234-017-120917  
; Sequence 120917, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 120917  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank U64445  
US-60-234-017-120917

Query Match 69.0%; Score 13.8; DB 55; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagt 17  
||| ||||| |||||  
Db 2 ctagggaagactcagt 18

RESULT 12  
US-60-234-017-120921  
; Sequence 120921, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILLING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 120921  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank U64445  
US-60-234-017-120921

Query Match 69.0%; Score 13.8; DB 55; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggggaggtcagt 17  
||| ||||| |||||  
Db 1 ctagggaagactcagt 17

RESULT 13  
PCT-US00-26619-18  
; Sequence 18, Application PC/TUS0026619  
; GENERAL INFORMATION:  
; APPLICANT: Meares, Claude  
; APPLICANT: Chmura, Albert  
; TITLE OF INVENTION: The Regents of the University of California  
; FILE REFERENCE: 023070-099120PC  
; CURRENT APPLICATION NUMBER: PCT/US00/26619  
; CURRENT FILLING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US 60/156,194  
; PRIOR FILLING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/208,684  
; PRIOR FILLING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:cloning primer  
; OTHER INFORMATION: with XhoI site  
PCT-US00-26619-18

Query Match 69.0%; Score 13.8; DB 1; Length 28;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggggaggtcagt 17  
||| ||||| |||||  
Db 12 ctgggggagactcagt 28

RESULT 14  
US-09-660-220-94301/c  
; Sequence 94301, Application US/09660220  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Affymetrix, Inc.



; TITLE OF INVENTION: Methods of Genetic Analysis of Human  
; FILE REFERENCE: 3102.1  
; CURRENT APPLICATION NUMBER: US/09/660,220  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/164,973  
; PRIOR FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 140981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 94301  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank U51003  
US-09-660-220-94301

Query Match 68.0%; Score 13.6; DB 26; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.9e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctaggaggagctcagtgtgg 20  
|||||  
Db 25 CTAGGGAGCCTCGTGTGG 6

## RESULT 15

US-08-305-771A-53  
; Sequence 53, Application US/08305771A  
; GENERAL INFORMATION:  
; APPLICANT: Barbara Sosnowski  
; APPLICANT: Lois Chandler  
; APPLICANT: L. L. Houston  
; APPLICANT: Michael Nova  
; TITLE OF INVENTION: CONJUGATES OF HEPARIN-BINDING EPIDERMAL  
; TITLE OF INVENTION: GROWTH FACTOR-LIKE GROWTH FACTOR AND TARGETED AGENTS  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/305,771A  
; FILING DATE: September 13, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/297,961  
; FILING DATE: 29-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/213,446  
; FILING DATE: 15-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/213,447  
; FILING DATE: 15-MAR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 519522  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-305-771A-53

Query Match 67.0%; Score 13.4; DB 7; Length 34;  
Best Local Similarity 93.3%; Pred. No. 2.4e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctaggggagggtcag 15  
|||||  
Db 11 CTATGGGAGGCTCAG 25

Search completed: October 2, 2001, 21:50:17  
Job time: 24530 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:04 ; Search time 2173.58 Seconds  
(without alignments)  
19.290 Million cell updates/sec

Title: US-09-757-100B-15

Perfect score: 20

Sequence: 1 ttgttggttccaatcgacc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2.6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2.6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2.6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2.6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 7: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 8: /cgn2.6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	13.2	66.0	32	7	US-09-724-671-20856
C 2	12.2	61.0	33	8	US-60-252-833-23017
C 3	12	60.0	20	6	US-09-198-452A-5586
C 4	12	60.0	48	8	US-60-253-653-5980
C 5	11.8	59.0	22	7	US-09-653-971A-4
C 6	11.8	59.0	35	6	US-09-882-246-29
C 7	11.4	57.0	25	5	US-09-623-025A-8
C 8	11.4	57.0	49	8	US-60-253-456-27270
C 9	11.2	56.0	20	6	US-09-198-452A-1694
C 10	11.2	56.0	20	6	US-09-198-452A-4752
C 11	11.2	56.0	38	8	US-60-253-378-10923
C 12	11.2	56.0	40	8	US-60-253-651-7574
C 13	11.2	56.0	50	7	PCT-US99-05606-8
C 14	11	55.0	24	7	US-09-730-559B-55
C 15	11	55.0	27	8	US-60-253-457-11420
C 16	11	55.0	28	8	US-09-574-376B-736
C 17	11	55.0	41	5	US-60-253-651-24602
C 18	11	55.0	44	8	US-60-253-378-10394
C 19	11	55.0	46	8	US-60-253-457-41965
C 20	11	55.0	50	8	US-09-198-452A-2476
C 21	10.8	54.0	20	6	US-09-752-110A-6
C 22	10.8	54.0	26	6	US-09-752-110A-9
C 23	10.8	54.0	28	6	US-09-882-246-27
C 24	10.8	54.0	35	6	US-60-253-654-8477
C 25	10.8	54.0	41	8	US-60-253-654-8477

ALIGNMENTS

RESULT 1

US-09-724-671-20856/c

; Sequence 20856, Application US/09724671

; GENERAL INFORMATION:

; APPLICANT: Watson, James D

; APPLICANT: Murison, James G

; TITLE OF INVENTION: Polynucleotides, polypeptides expressed

; FILE REFERENCE: 105002

; CURRENT APPLICATION NUMBER: US/09724,671

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678

; NUMBER OF SEQ ID NOS: 21907

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 20856

; LENGTH: 32

; TYPE: DNA

; ORGANISM: Mouse

US-09-724-671-20856

Query Match 66.0%; Score 13.2; DB 7; Length 32;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ttggttccaatcgacc 20

DB 32 TCGGCTTCCAATAGGACC 15

RESULT 2

US-60-252-833-23017

; Sequence 23017, Application US/60252833

; GENERAL INFORMATION:

; APPLICANT: Glenn, Matthew

; APPLICANT: Grigor, Murray R

; TITLE OF INVENTION: Compositions isolated from bovine

; FILE REFERENCE: 1052P2

; CURRENT APPLICATION NUMBER: US/60/252,833

; CURRENT FILING DATE: 2000-11-21

; NUMBER OF SEQ ID NOS: 43535

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 23017

; LENGTH: 33

; TYPE: DNA

; ORGANISM: Bovine

Sequence 8477, Ap  
Sequence 14850, A  
Sequence 1727, Ap  
Sequence 3091, Ap  
Sequence 2642, Ap  
Sequence 2643, Ap  
Sequence 46, Appl  
Sequence 41, Appl  
Sequence 2875, Ap  
Sequence 5086, Ap  
Sequence 7, Appl  
Sequence 1225, Ap  
Sequence 256, App  
Sequence 256, App  
Sequence 7833, Ap  
Sequence 7431, Ap  
Sequence 7431, Ap  
Sequence 15900, A  
Sequence 34, Appl

RESULT 5  
US-09-653-971A-4/C  
; Sequence 4, Application US/09653971A  
; GENERAL INFORMATION:  
; APPLICANT: DUCKWORTH, DAVID MALCOLM

APPLICATION NUMBER: 07/536,428

; FILING DATE: 11 JUNE 1990  
; APPLICATION NUMBER: 07/931,473  
; FILING DATE: 17 AUGUST 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX10/US-CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-882-246-29

Query Match 59.0%; Score 11.8; DB 6; Length 35;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ttgttggttccaac 15  
Db 18 UGUUUGUUCACUC 32

RESULT 7  
US-09-623-025A-8/c  
; Sequence 8, Application US/09623025A  
; GENERAL INFORMATION:  
; APPLICANT: University of Nevada-Reno, Richard Bjur, PhD, JD  
; TITLE OF INVENTION: Identification of Oxidant Isoform of Human MnSOD  
; FILE REFERENCE: unevadreno5013  
; CURRENT APPLICATION NUMBER: US/09/623,025A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: PCT/US99/04129  
; PRIOR FILING DATE: 1998-02-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: oligonucleotide  
US-09-623-025A-8

Query Match 57.0%; Score 11.4; DB 6; Length 25;  
Best Local Similarity 92.3%; Pred. No. 1e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ttgttggttccaac 13  
Db 24 TGTGTGTGTCAC 12

RESULT 8  
US-60-253-456-27270  
; Sequence 27270, Application US/60253456  
; GENERAL INFORMATION:  
; APPLICANT: Havukkala, Ilkka J  
; TITLE OF INVENTION: Polynucleotides, isolated from  
; FILE REFERENCE: 1054P1  
; CURRENT APPLICATION NUMBER: US/60/253,456  
; CURRENT FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 37096  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27270  
; LENGTH: 49  
; TYPE: DNA

; ORGANISM: Pinus radiata  
US-60-253-456-27270

Query Match 57.0%; Score 11.4; DB 8; Length 49;  
Best Local Similarity 92.3%; Pred. No. 1.1e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttgttggttccaac 15  
Db 1 ttggttccaac 13

RESULT 9  
US-09-198-452A-1694/c  
; Sequence 1694, Application US/09198452A  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 1694  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-1694

Query Match 56.0%; Score 11.2; DB 6; Length 20;  
Best Local Similarity 81.2%; Pred. No. 1.3e+04;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ggtttccaactcgacc 20  
Db 19 GGTTCACAAATTGCC 4

RESULT 10  
US-09-198-452A-4752/c  
; Sequence 4752, Application US/09198452A  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 4752  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-4752

Query Match 56.0%; Score 11.2; DB 6; Length 20;  
Best Local Similarity 81.2%; Pred. No. 1.3e+04;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggttccaactcg 17  
Db 17 GTTGATACAAATCG 2

RESULT 11  
US-60-253-378-10923  
; Sequence 10923, Application US/60253378  
; GENERAL INFORMATION:

; APPLICANT: Havukkala, Ilkka J  
; TITLE OF INVENTION: Polynucleotides isolated from plants  
; FILE OF INVENTION: and methods for their use.  
; FILE REFERENCE: 1054P3  
; CURRENT APPLICATION NUMBER: US/60/253,378  
; CURRENT FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 40367  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10923  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-60-253-378-10923

Query Match 56.0%; Score 11.2; DB 8; Length 38;  
Best Local Similarity 81.2%; Pred. No. 1.4e+04;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ttgtgtttcccaatcg 16  
||||| ||||| |||  
Db 19 ttgtgtttccctagcg 34

## RESULT 12

US-60-253-651-7574  
; Sequence 7574, Application US/60253651  
; GENERAL INFORMATION:

; APPLICANT: Glenn, Matthew  
; APPLICANT: Grigor, Murray R  
; TITLE OF INVENTION: Compositions isolated from bovine tissue  
; FILE OF INVENTION: and methods for their use.  
; FILE REFERENCE: 1055P3  
; CURRENT APPLICATION NUMBER: US/60/253,651  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 27858  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7574  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Bovine  
US-60-253-651-7574

Query Match 56.0%; Score 11.2; DB 8; Length 40;  
Best Local Similarity 81.2%; Pred. No. 1.4e+04;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ttgtgtttcccaatcgga 18  
||| ||||| |||||  
Db 25 ttgactttccaaacgga 40

## RESULT 13

US-09-822-698A-14/c

; Sequence 14, Application US/09822698A  
; GENERAL INFORMATION:

; APPLICANT: Hendrickx, Maria P.G.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DYA-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 14  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:

; OTHER INFORMATION: VL forward primer for light chain variable region

; OTHER INFORMATION: of PH1 Fab antibody with additional linker and  
; OTHER INFORMATION: restriction sites  
US-09-822-698A-14

Query Match 56.0%; Score 11.2; DB 7; Length 50;  
Best Local Similarity 81.2%; Pred. No. 1.5e+04;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttgggtttcccaatcg 17  
||| ||||| |||||  
Db 32 GTGGATATCCAATCGG 17

## RESULT 14

PCT-US99-05606-8

; Sequence 8, Application PC/TUS9905606  
; GENERAL INFORMATION:  
; APPLICANT: Millenium Pharmaceuticals, Inc.  
; APPLICANT: Regents of the University of California  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS  
; FILE REFERENCE: 7853-138-228  
; CURRENT APPLICATION NUMBER: PCT/US99/05606  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/236,134  
; PRIOR FILING DATE: 1999-01-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
PCT-US99-05606-8

Query Match 55.0%; Score 11; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 gttgggtttccca 12  
||||| |||||  
Db 5 gttgggtttccca 15

## RESULT 15

US-09-730-559B-55

; Sequence 55, Application US/09730559B  
; GENERAL INFORMATION:

; APPLICANT: ISHIWATA, TETSUYOSHI  
; APPLICANT: SAKURADA, MIKIO  
; APPLICANT: KAWABATA, AYAKO  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: NISHI, TATSUNARI  
; APPLICANT: KUGA, TETSURO  
; APPLICANT: SAWADA, SHIGEMASA  
; APPLICANT: TAKEI, MASAMI  
; APPLICANT: SHIBATA, KENJI  
; APPLICANT: FURUYA, AKIO  
; TITLE OF INVENTION: Iga NEPHROPATHY-ASSOCIATED GENE  
; FILE REFERENCE: 766.21 CIP  
; CURRENT APPLICATION NUMBER: US/09/730,559B  
; CURRENT FILING DATE: 2000-12-07  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA

US-09-730-559B-55

Query Match 55.0%; Score 11; DB 7; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 t g t t g g t t t c c a a t c g g a c 19  
||| ||| ||| ||| |||  
Db 3 t g a t g c t t t t c t a t c t g a c 21

Search completed: October 2, 2001, 16:55:04  
Job time: 17667 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:15 ; Search time 17695.9 Seconds  
(without alignments)  
16.701 Million cell updates/sec

Title: US-09-757-100B-15  
Perfect score: 20  
Sequence: 1 tgttggtttccaatcgacc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues  
Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

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- 2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*
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- 4: /cgn2\_6/ptodata/1/pna/US08\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*
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- 15: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pna/US092\_COMB.seq.\*
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- 19: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*
- 23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*
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- 34: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq.\*
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- 36: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq.\*
- 37: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq.\*
- 38: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq.\*
- 39: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq.\*
- 40: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*
- 41: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq.\*
- 42: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq.\*
- 43: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq.\*
- 44: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq.\*

- 44: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*
- 45: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq.\*
- 46: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq.\*
- 47: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq.\*
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- 52: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq.\*
- 53: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*
- 54: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*
- 55: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq.\*
- 56: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*
- 57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*
- 58: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*
- 59: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*
- 60: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	100.0	20	1	PCT-US000-18999-15	Sequence 15, Appl
2	20	100.0	20	17	US-09-377-100B-15	Sequence 15, Appl
3	20	100.0	20	29	US-09-757-100B-15	Sequence 15, Appl
C 4	15.8	79.0	25	55	US-60-234-017-154082	Sequence 154082,
C 5	15.2	76.0	25	55	US-60-233-620-7572	Sequence 7572, Ap
C 6	15.2	76.0	25	55	US-60-234-017-201094	Sequence 201094,
7	15	75.0	15	1	PCT-US000-18999-35	Sequence 35, Appl
8	15	75.0	15	17	US-09-377-310-35	Sequence 35, Appl
9	15	75.0	15	29	US-09-757-100B-35	Sequence 35, Appl
C 10	14.2	71.0	25	55	US-60-233-620-1645	Sequence 1645, Ap
C 11	14.2	71.0	25	55	US-60-234-017-42731	Sequence 42731, A
C 12	14.2	71.0	25	55	US-60-234-017-42735	Sequence 42735, A
C 13	14.2	71.0	25	55	US-60-234-017-196005	Sequence 196005,
C 14	14.2	71.0	25	55	US-60-234-017-216701	Sequence 216701,
C 15	13.8	69.0	25	55	US-60-232-638-33957	Sequence 33957, A
C 16	13.8	69.0	25	55	US-60-233-166-79738	Sequence 79738, A
C 17	13.8	69.0	41	18	US-09-404-520-38668	Sequence 38668, A
C 18	13.6	68.0	25	26	US-09-660-220-65925	Sequence 65925, A
C 19	13.6	68.0	25	55	US-60-232-638-137242	Sequence 137242,
C 20	13.6	68.0	25	55	US-60-233-166-184627	Sequence 184627,
C 21	13.6	68.0	46	13	US-08-983-474-6	Sequence 6, Appl
C 22	13.6	68.0	46	13	US-08-983-474A-6	Sequence 6, Appl
C 23	13.4	67.0	25	55	US-60-234-017-261020	Sequence 261020,
C 24	13.2	66.0	25	55	US-60-232-638-69603	Sequence 69603, A
C 25	13.2	66.0	25	55	US-60-232-638-131648	Sequence 131648,
C 26	13.2	66.0	25	55	US-60-232-638-131659	Sequence 131659,
C 27	13.2	66.0	25	55	US-60-233-166-258281	Sequence 258281,
C 28	13.2	66.0	25	55	US-60-233-166-266921	Sequence 266921,
C 29	13.2	66.0	25	55	US-60-233-166-408428	Sequence 408428,
C 30	13.2	66.0	25	55	US-60-234-017-167542	Sequence 167542,
C 31	13.2	66.0	25	55	US-60-234-017-209729	Sequence 209729,
C 32	13.2	66.0	25	55	US-60-234-017-275344	Sequence 275344,
C 33	13.2	66.0	25	55	US-60-234-017-476537	Sequence 476537,
C 34	13.2	66.0	25	55	US-60-234-049-30000	Sequence 30000, A
C 35	13.2	66.0	26	10	US-08-624-655A-6	Sequence 6, Appl
C 36	13.2	66.0	47	18	US-09-422-978-3652	Sequence 3652, Ap
C 37	13	65.0	25	55	US-60-233-620-122282	Sequence 122282,
C 38	13	65.0	25	55	US-60-234-017-218413	Sequence 218413,
C 39	13	65.0	25	55	US-60-234-017-218414	Sequence 218414,
C 40	12.8	64.0	18	28	US-09-422-978-5568	Sequence 5568, Ap
C 41	12.8	64.0	20	28	US-09-703-708-17795	Sequence 17795, A
C 42	12.8	64.0	20	48	US-60-164-320-17795	Sequence 17795, A
C 43	12.8	64.0	20	50	US-60-183-791-17795	Sequence 34480, A
C 44	12.8	64.0	25	26	US-09-660-220-34480	Sequence 84625, A
C 45	12.8	64.0	25	55	US-60-234-049-84625	

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-15  
; Sequence 15, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-15

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcggacc 20  
|||||  
Db 1 tgggtgttccaatcggacc 20

RESULT 2  
US-09-377-310-15  
; Sequence 15, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-15

Query Match 100.0%; Score 20; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcggacc 20  
|||||  
Db 1 tgggtgttccaatcggacc 20

RESULT 3  
US-09-757-100B-15  
; Sequence 15, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-15

Query Match 100.0%; Score 20; DB 29; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcggacc 20  
|||||  
Db 1 tgggtgttccaatcggacc 20

RESULT 4  
US-60-234-017-154082/c  
; Sequence 154082, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 154082  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AI854607  
US-60-234-017-154082

Query Match 79.0%; Score 15.8; DB 55; Length 25;  
Best Local Similarity 89.5%; Pred. No. 4.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcggacc 19  
|||||  
Db 19 TGTGTTTCAATCGAAC 1

RESULT 5  
US-60-233-620-7572/c  
; Sequence 7572, Application US/60233620  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of  
; FILE REFERENCE: Arabidopsis thaliana  
; FILE REFERENCE: 3116

; CURRENT APPLICATION NUMBER: US/60/233,620  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 131820  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7572  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AC003028  
US-60-233-620-7572

Query Match 76.0%; Score 15.2; DB 55; Length 25;  
Best Local Similarity 85.0%; Pred. No. 9.8e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ttgtgtttccaatcgacc 20  
Db 25 TCTGTGTTTCCACTCCGACC 6

RESULT 6  
US-60-234-017-201094/c  
; Sequence 201094, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 201094  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA792731  
US-60-234-017-201094

Query Match 76.0%; Score 15.2; DB 55; Length 25;  
Best Local Similarity 85.0%; Pred. No. 9.8e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ttgtgtttccaatcgacc 20  
Db 25 TGTGTGTTATCCACAGGACC 6

RESULT 7  
PCT-US00-18999-35  
; Sequence 35, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 15  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-35

Query Match 75.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttggtttccaatcg 17  
Db 1 ttggtttccaatcg 15

RESULT 8  
US-09-377-310-35  
; Sequence 35, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-35

Query Match 75.0%; Score 15; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttggtttccaatcg 17  
Db 1 ttggtttccaatcg 15

RESULT 9  
US-09-757-100B-35  
; Sequence 35, Application US/09757100B  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-35

Query Match 75.0%; Score 15; DB 29; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ttgggtttccaatcgg 17  
||||| ||||| |||||

Db 1 ttgggtttccaatcgg 15

## RESULT 10

US-60-233-620-1645/c

; Sequence 1645, Application US/60233620

; GENERAL INFORMATION:

; APPLICANT: Mittmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of

; FILE OF INVENTION: Arabidopsis thaliana

; FILE REFERENCE: 3116

; CURRENT APPLICATION NUMBER: US/60/233,620

; CURRENT FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 131820

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1645

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AC000132

US-60-233-620-1645

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20  
||||| ||||| |||||

Db 23 GTTCGTTACCAATAGACC 5

## RESULT 11

US-60-234-017-42731/c

; Sequence 42731, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE OF INVENTION: musculus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 42731

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank L03215

US-60-234-017-42731

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20  
||||| ||||| |||||

Db 23 GTTCGTTACCAATAGACC 5

## RESULT 12

US-60-234-017-42735/c

; Sequence 42735, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE OF INVENTION: musculus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 42735

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank L03215

US-60-234-017-42735

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20  
||||| ||||| |||||

Db 19 GTTCGTTCCCGATCGGACC 1

## RESULT 13

US-60-234-017-196005/c

; Sequence 196005, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE OF INVENTION: musculus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 196005

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AAL75641

US-60-234-017-196005

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20  
||||| ||||| |||||

Db 25 GTTCGTTCCCGATCGGACC 7

## RESULT 14

US-60-234-017-216701

; Sequence 216701, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE OF INVENTION: musculus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 216701  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AY789319  
US-60-234-017-216701

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 ttgtgtttccaatcgacc 20  
||||| | ||||| |  
Db 1 ttgtgtttacgacgtgcc 19

RESULT 15  
US-60-232-638-33957/c  
; Sequence 33957; Application US/60232638  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
; FILE REFERENCE: 3110  
; CURRENT APPLICATION NUMBER: US/60/232,638  
; CURRENT FILING DATE: 2000-09-14  
; NUMBER OF SEQ ID NOS: 138410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33957  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SGD YBR001C  
US-60-232-638-33957

Query Match 69.0%; Score 13.8; DB 55; Length 25;  
Best Local Similarity 88.2%; Pred. No. 5.5e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 ttgtttccaatcgacc 20  
||||| | ||||| |  
Db 20 TGGTTTATATCGGACC 4

Search completed: October 2, 2001, 21:50:16  
Job time: 24529 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:03 ; Search time 2173.58 Seconds  
(without alignments)  
19,290 Million cell updates/sec

Title: US-09-757-100B-14

Perfect score: 20

Sequence: 1 ggttagggatggtgcgcgtca 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq1.\*  
7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq2.\*  
8: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.6	63.0	32	7	US-09-735-271-1541
C 2	12.6	63.0	33	7	US-09-672-217-151
C 3	12.6	63.0	33	7	US-09-672-217-253
C 4	12.6	63.0	37	5	US-09-536-784-339
C 5	12.6	63.0	37	6	US-09-765-272-339
C 6	12.4	62.0	31	5	US-09-574-376B-1253
C 7	12.2	61.0	21	6	US-09-715-849-504
C 8	12.0	60.0	38	5	US-09-371-772B-7196
C 9	12.0	60.0	38	5	US-09-371-772B-10090
C 10	12.0	60.0	38	5	US-09-708-690-9473
C 11	12.0	60.0	38	5	US-09-708-690-12367
C 12	11.8	59.0	31	7	US-09-840-424-947
C 13	11.8	59.0	33	7	US-09-908-744-61
C 14	11.6	58.0	26	8	US-60-253-654-14371
C 15	11.6	58.0	26	8	US-60-255-592-14371
C 16	11.4	57.0	19	6	US-09-375-318-65
C 17	11.4	57.0	21	6	US-09-508-891-1
C 18	11.4	57.0	45	7	US-09-908-827-27
C 19	11.2	56.0	43	8	US-60-253-651-1558
C 20	11.0	55.0	30	7	US-09-890-997-3
C 21	11.0	55.0	32	6	US-09-787-097-5
C 22	11.0	55.0	36	5	US-09-274-553C-1747
C 23	11.0	55.0	36	5	US-09-406-643-1833
C 24	11.0	55.0	37	6	US-09-546-745A-7011
C 25	11.0	55.0	37	7	US-09-735-271-1542

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26 11 55.0 38 5 US-09-371-772B-7552 Sequence 7552, Ap
27 11 55.0 38 5 US-09-371-772B-8141 Sequence 8141, Ap
28 11 55.0 38 5 US-09-371-772B-9645 Sequence 9645, Ap
29 11 55.0 38 5 US-09-371-772B-10487 Sequence 10487, A
30 11 55.0 38 5 US-09-371-772B-10818 Sequence 10818, A
31 11 55.0 38 5 US-09-371-772B-10877 Sequence 10877, A
32 11 55.0 38 5 US-09-371-772B-11311 Sequence 11311, A
33 11 55.0 38 5 US-09-371-772B-11364 Sequence 11364, A
34 11 55.0 38 5 US-09-371-772B-12297 Sequence 12297, A
35 11 55.0 38 5 US-09-371-772B-12605 Sequence 12605, A
36 11 55.0 38 5 US-09-371-772B-13335 Sequence 13335, A
37 11 55.0 38 5 US-09-708-690-9829 Sequence 9829, Ap
38 11 55.0 38 5 US-09-708-690-10418 Sequence 10418, A
39 11 55.0 38 5 US-09-708-690-11922 Sequence 11922, A
40 11 55.0 38 5 US-09-708-690-12764 Sequence 12764, A
41 11 55.0 38 5 US-09-708-690-13095 Sequence 13095, A
42 11 55.0 38 5 US-09-708-690-13154 Sequence 13154, A
43 11 55.0 38 5 US-09-708-690-13588 Sequence 13588, A
44 11 55.0 38 5 US-09-708-690-13641 Sequence 13641, A
45 11 55.0 38 5 US-09-708-690-14574 Sequence 14574, A

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## ALIGNMENTS

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RESULT 1
US-09-735-271-1541/c
; Sequence 1541, Application US/09735271
; GENERAL INFORMATION:
; APPLICANT: Daly, Mark J.
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Lander, Eric S.
; APPLICANT: Rioux, John
; APPLICANT: Siminovich, Kathy
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS
; FILE REFERENCE: 2825.1025-002
; CURRENT APPLICATION NUMBER: US/09/735,271
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/170,257
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1541
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(32)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1541

Query Match 63.0%; Score 12.6; DB 7; Length 32;
Best Local Similarity 75.0%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgcgtca 20
   ||| ||| ||| ||| |||
Db 22 GGTANGGACGCGTGCATCA 3

RESULT 2
US-09-672-217-151
; Sequence 151, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; APPLICANT: MCCABE, MEADE
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143

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; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 151
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-151

Query Match          63.0%; Score 12.6; DB 7; Length 33;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgcgtca 20
   ||| ||| ||| ||| |||
Db 15 gttggtgaaggtgcagtc 33

RESULT 3
US-09-672-217-253
; Sequence 253, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; APPLICANT: MCCABE, MEADE
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143
; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 253
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-253

Query Match          63.0%; Score 12.6; DB 7; Length 33;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgcgtca 20
   ||| ||| ||| ||| |||
Db 15 gttggtgaaggtgcagtc 33

RESULT 4
US-09-536-784-339/c
; Sequence 339, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
```

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; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 339:
US-09-536-784-339

Query Match          63.0%; Score 12.6; DB 5; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgcgtca 20
   ||| ||| ||| ||| |||
Db 19 GCTAGCGATGGATCCGTCA 1

RESULT 5
US-09-765-272-339/c
; Sequence 339, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
```



; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 339:  
US-09-765-272-339

Query Match 63.0%; Score 12.6; DB 6; Length 37;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgtca 20  
||| ||||| |||||  
DB 19 GCTAGGATGGATCCGTCA 1

RESULT 6  
US-09-574-376B-1253/c  
; Sequence 1253, Application US/09574376B  
; GENERAL INFORMATION:  
; APPLICANT: Warrington, Janet  
; APPLICANT: Shah, Nila  
; APPLICANT: Gingeras, Thomas Raymond  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms  
; FILE REFERENCE: 3229.2  
; CURRENT APPLICATION NUMBER: US/09/574, 376B  
; CURRENT FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 1330  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1253  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
US-09-574-376B-1253

Query Match 62.0%; Score 12.4; DB 5; Length 31;  
Best Local Similarity 81.2%; Pred. No. 5.6e+03;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ttaggatggtgcgt 18  
||| ||||| |||||  
DB 27 TTGGGGATGGARCCGT 12

RESULT 7  
US-09-715-849-504/c  
; Sequence 504, Application US/09715849  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: 2825.2002-001  
; CURRENT APPLICATION NUMBER: US/09/715, 849  
; CURRENT FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/167, 334  
; PRIOR FILING DATE: 1999-11-24  
; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 504  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-715-849-504

Query Match 61.0%; Score 12.2; DB 6; Length 21;  
Best Local Similarity 73.7%; Pred. No. 6.8e+03;  
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgtc 19

DB 19 GGTGAGGGMGGTGCAGGC 1  
||| ||||| ||||| |||

RESULT 8  
US-09-371-772B-7196  
; Sequence 7196, Application US/09371772B  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions  
; FILE REFERENCE: MBHB00, 876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371, 772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005, 974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584, 040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7196  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-7196

Query Match 60.0%; Score 12; DB 5; Length 38;  
Best Local Similarity 55.0%; Pred. No. 9.3e+03;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgtca 20  
||| ||||| ||||| |||  
DB 4 gguacugaugagcgcuua 23

RESULT 9  
US-09-371-772B-10090  
; Sequence 10090, Application US/09371772B  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions  
; FILE REFERENCE: MBHB00, 876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371, 772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005, 974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584, 040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10090  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-10090

Query Match 60.0%; Score 12; DB 5; Length 38;  
Best Local Similarity 55.0%; Pred. No. 9.3e+03;

Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgcgtca 20  
||:| ||:| ||||:|  
Db 4 gguuacugaugagggccguua 23

## RESULT 10

US-09-708-690-9473  
; Sequence 9473, Application US/09708690  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-L (400/002)  
; CURRENT APPLICATION NUMBER: US/09/708,690  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9473  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-708-690-9473

Query Match 60.0%; Score 12; DB 5; Length 38;  
Best Local Similarity 55.0%; Pred. No. 9.3e+03;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgcgtca 20  
||:| ||:| ||||:|  
Db 4 gguuacugaugagggccguua 23

## RESULT 11

US-09-708-690-12367  
; Sequence 12367, Application US/09708690  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-L (400/002)  
; CURRENT APPLICATION NUMBER: US/09/708,690  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12367  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-708-690-12367

Query Match 60.0%; Score 12; DB 5; Length 38;  
Best Local Similarity 55.0%; Pred. No. 9.3e+03;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgcgtca 20  
||:| ||:| ||||:|  
Db 4 gguuacugaugagggccguua 23

## RESULT 12

US-09-840-424-947  
; Sequence 947, Application US/09840424  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
; TITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY  
; FILE REFERENCE: 1600,1010-002  
; CURRENT APPLICATION NUMBER: US/09/840,424  
; CURRENT FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: US 60/084,098  
; PRIOR FILING DATE: 1998-05-04  
; PRIOR APPLICATION NUMBER: US 60/123,523  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: US 60/126,974  
; PRIOR FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: US 09/304,649  
; PRIOR FILING DATE: 1999-05-04  
; NUMBER OF SEQ ID NOS: 1311  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 947  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(31)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-840-424-947

Query Match 59.0%; Score 11.8; DB 7; Length 31;  
Best Local Similarity 81.2%; Pred. No. 1.2e+04;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tagggatggtgcgcgtc 19  
|| | ||||| |||  
Db 3 taagnatggtgctgtc 18

## RESULT 13

US-09-908-744-61  
; Sequence 61, Application US/09908744  
; GENERAL INFORMATION:  
; APPLICANT: Miasnikov Andrei  
; APPLICANT: Ojamo Heikki  
; APPLICANT: Povelainen Mira  
; APPLICANT: Gros H+kan  
; APPLICANT: Toivari Mervi  
; APPLICANT: Richon Peter  
; APPLICANT: Ruohonen Laura  
; APPLICANT: Koivuranta Kari  
; APPLICANT: Lonsborough John  
; APPLICANT: Aristidou Aristos

```
; APPLICANT: Penttil, Merja
; APPLICANT: Plazanet-Menut Claire
; APPLICANT: Deutscher Josef
; TITLE OF INVENTION: Manufacture of Five-Carbon Sugars and Sugar Alcohols
; FILE REFERENCE: 1427 0010005
; CURRENT APPLICATION NUMBER: US/09/908,744
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: PCT/FI01/00051
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/488,581
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 08/790,585
; PRIOR FILING DATE: 1997-01-29
; PRIOR APPLICATION NUMBER: US 08/368,395
; PRIOR FILING DATE: 1995-01-03
; PRIOR APPLICATION NUMBER: US 08/110,672
; PRIOR FILING DATE: 1993-08-24
; PRIOR APPLICATION NUMBER: US 07/973,325
; PRIOR FILING DATE: 1992-11-05
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 61
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OGDH3 primer
US-09-908-744-61
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Query Match 59.0%; Score 11.8; DB 7; Length 33;
Best Local Similarity 86.7%; Pred. NO. 1.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 agggatggtgcgcgc 19
|| ||||| |||
Db 19 agcgatggtgcgc 33
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RESULT 14
US-60-253-654-14371/c
; Sequence 14371, Application US/60253654
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Norriss, Michael G.
; TITLE OF INVENTION: Compositions isolated from forage
; TITLE OF INVENTION: grasses and methods for their use.
; FILE REFERENCE: 1056P
; CURRENT APPLICATION NUMBER: US/60/253,654
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 32581
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14371
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Festuca arundinaceae
US-60-253-654-14371
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Query Match 58.0%; Score 11.6; DB 8; Length 26;
Best Local Similarity 77.8%; Pred. NO. 1.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ttaggatggtgcgcgc 20
|| ||||| |||
Db 18 TTTTGGATGGTTCGGTCA 1
```

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RESULT 15
US-60-255-592-14371/c
; Sequence 14371, Application US/60255592
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
```

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; APPLICANT: Norriss, Michael G.
; TITLE OF INVENTION: Compositions isolated from forage
; FILE REFERENCE: 1056P2
; CURRENT APPLICATION NUMBER: US/60/255,592
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 32581
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14371
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Festuca arundinaceae
US-60-255-592-14371

Query Match 58.0%; Score 11.6; DB 8; Length 26;
Best Local Similarity 77.8%; Pred. NO. 1.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ttaggatggtgcgcgc 20
|| ||||| |||
Db 18 TTTTGGATGGTTCGGTCA 1

Search completed: October 2, 2001, 16:55:04
Job time: 17667 sec
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run On: October 2, 2001, 21:50:15 ; Search time 17695.9 Seconds  
(without alignments)  
16.701 Million cell updates/sec

Title: US-09-757-100B-14

Perfect score: 20

Sequence: 1 ggtagggatggtgcgcgtca 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 53: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*
- 54: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*
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- 56: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*
- 57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	1	PCT-US00-18999-14	Sequence 14, Appl
2	20	100.0	20	17	US-09-377-310-14	Sequence 14, Appl
3	20	100.0	20	29	US-09-757-100B-14	Sequence 14, Appl
c	15.2	76.0	25	55	US-60-233-166-198784	Sequence 138784,
4	15	75.0	15	1	PCT-US00-18999-34	Sequence 34, Appl
5	15	75.0	15	17	US-09-377-310-34	Sequence 34, Appl
6	15	75.0	15	29	US-09-757-100B-34	Sequence 34, Appl
7	15	75.0	15	26	US-09-660-220-13935	Sequence 13935, A
8	14.2	71.0	25	55	US-60-232-638-39603	Sequence 39603, A
c	14.2	71.0	25	55	US-60-233-620-79723	Sequence 79723, A
9	14.2	71.0	25	55	US-60-234-017-255450	Sequence 255450,
10	14.2	71.0	34	14	US-09-004-729-58	Sequence 58, Appl
11	14.2	71.0	34	15	US-09-004-755-58	Sequence 58, Appl
12	14.2	71.0	34	15	US-09-171-741C-58	Sequence 58, Appl
13	14.2	71.0	34	15	US-09-171-741C-58	Sequence 1, Appl
14	14.2	71.0	34	15	US-09-171-741C-58	Sequence 1, Appl
c	13.8	69.0	24	3	US-07-896-094-1	Sequence 18, Appl
15	13.8	69.0	24	8	US-08-458-319-18	Sequence 18, Appl
16	13.8	69.0	25	26	US-09-660-220-118931	Sequence 118931,
17	13.8	69.0	25	26	US-60-234-017-472694	Sequence 472694,
18	13.8	69.0	25	55	US-60-234-017-472694	Sequence 141254,
19	13.8	69.0	25	55	US-60-234-049-141254	Sequence 141254,
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20	13.6	68.0	25	55	US-60-233-166-62879	Sequence 285311,
21	13.6	68.0	25	55	US-60-233-166-285311	Sequence 285311,
22	13.6	68.0	25	55	US-60-233-166-285312	Sequence 285312,
23	13.6	68.0	25	55	US-60-233-166-285313	Sequence 285313,
24	13.6	68.0	25	55	US-60-233-166-285315	Sequence 285315,
25	13.6	68.0	25	55	US-60-234-017-336370	Sequence 336370,
26	13.6	68.0	25	55	US-60-234-049-88046	Sequence 88046, A
c	13.4	67.0	18	1	PCT-US99-08268-120	Sequence 120, App
27	13.4	67.0	18	1	PCT-US99-08268-121	Sequence 121, App
28	13.4	67.0	18	1	PCT-US99-09085-11	Sequence 11, Appl
29	13.4	67.0	18	1	PCT-US99-09085-12	Sequence 12, Appl
30	13.4	67.0	18	16	US-09-295-463-120	Sequence 120, App
c	13.4	67.0	18	16	US-09-295-463-121	Sequence 121, App
31	13.4	67.0	18	17	US-09-387-341-113	Sequence 113, App
32	13.4	67.0	18	17	US-09-387-341-114	Sequence 114, App
33	13.4	67.0	25	55	US-60-233-166-32127	Sequence 32127, A
34	13.2	66.0	25	55	US-60-233-166-69850	Sequence 69850, A
35	13.2	66.0	25	55	US-60-233-166-94414	Sequence 94414, A
c	13.2	66.0	25	55	US-60-233-166-352745	Sequence 352745, A
36	13.2	66.0	25	55	US-60-233-620-59155	Sequence 59155, A
37	13.2	66.0	25	55	US-60-234-017-199517	Sequence 199517,
38	13.2	66.0	25	55	US-60-234-017-590747	Sequence 590747,
39	13.2	66.0	33	3	US-07-958-143A-98	Sequence 98, Appl
40	13.2	66.0	33	4	US-08-057-165-98	Sequence 98, Appl
41	13.2	66.0	40	25	US-09-645-706-147	Sequence 147, App
c	13.2	66.0	40	25	US-60-234-049-138406	Sequence 138406,
42	12.8	64.0	25	55		

## ALIGNMENTS

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RESULT 1
PCT-US00-18999-14
; Sequence 14, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-14

Query Match          100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
   |||||
Db 1 ggttagggatggtgccgtca 20

RESULT 2
US-09-377-310-14
; Sequence 14, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-14

Query Match          100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
   |||||
Db 1 ggttagggatggtgccgtca 20

RESULT 3
US-09-757-100b-14
; Sequence 14, Application US/09757100B
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; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-14

Query Match          100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
   |||||
Db 1 ggttagggatggtgccgtca 20

RESULT 4
US-60-233-166-198784/c
; Sequence 198784, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-60-233-166-198784

Query Match          76.0%; Score 15.2; DB 55; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
   |||||
Db 25 GGTAGAGATGGATCCGTCA 6

RESULT 5
PCT-US00-18999-34
; Sequence 34, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
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; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-34

Query Match 75.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttagggtggtgcgcg 17  
|||||  
Db 1 ttagggtggtgcgcg 15

RESULT 6  
US-09-377-310-34  
; Sequence 34, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-34

Query Match 75.0%; Score 15; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttagggtggtgcgcg 17  
|||||  
Db 1 ttagggtggtgcgcg 15

RESULT 7  
US-09-757-100B-34  
; Sequence 34, Application US/09757100B  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-34

Query Match 75.0%; Score 15; DB 29; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttagggtggtgcgcg 17  
|||||  
Db 1 ttagggtggtgcgcg 15

RESULT 8  
US-09-660-220-13935  
; Sequence 13935, Application US/09660220  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann et al.  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Human  
; FILE REFERENCE: 3102.1  
; CURRENT APPLICATION NUMBER: US/09/660,220  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/164,973  
; PRIOR FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 140981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13935  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank D83784  
US-09-660-220-13935

Query Match 71.0%; Score 14.2; DB 26; Length 25;  
Best Local Similarity 84.2%; Pred. No. 8.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgcgc 19  
|||||  
Db 1 ggttagggatggtgcgcgc 19

RESULT 9  
US-60-232-638-39603/c  
; Sequence 39603, Application US/60232638  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
; FILE REFERENCE: 3110  
; CURRENT APPLICATION NUMBER: US/60/232,638  
; CURRENT FILING DATE: 2000-09-14  
; NUMBER OF SEQ ID NOS: 138410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 39603  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SGD YCLO29C  
US-60-232-638-39603

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
 Best Local Similarity 84.2%; Pred. No. 8.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ggttagggatggtccgctc 19  
 ||||| || ||||| ||||| |||||  
 Db 24 GGTAGGATGTCGCCGTC 6

## RESULT 10

US-60-233-620-79723/c  
 ; Sequence 79723, Application US/60233620  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mittmann  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of  
 ; TITLE OF INVENTION: Arabidopsis thaliana  
 ; FILE REFERENCE: 3116  
 ; CURRENT APPLICATION NUMBER: US/60/233,620  
 ; CURRENT FILING DATE: 2000-10-24  
 ; NUMBER OF SEQ ID NOS: 131820  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 79723  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank AC005168  
 US-60-233-620-79723

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
 Best Local Similarity 84.2%; Pred. No. 8.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 gttaggatggtccgctca 20  
 ||||| ||||| ||||| |||||  
 Db 25 GTTAGGATGTCCTTCA 7

## RESULT 11

US-60-234-017-255450  
 ; Sequence 255450, Application US/60234017  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mittmann, M  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
 ; TITLE OF INVENTION: musculus  
 ; FILE REFERENCE: 3115  
 ; CURRENT APPLICATION NUMBER: US/60/234,017  
 ; CURRENT FILING DATE: 2000-09-20  
 ; NUMBER OF SEQ ID NOS: 605887  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 255450  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank AW125675  
 US-60-234-017-255450

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
 Best Local Similarity 84.2%; Pred. No. 8.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ggttagggatggtccgctc 19  
 ||||| ||||| ||||| |||||  
 Db 1 ggttagggatggtccgctc 19

## RESULT 12

US-09-004-729-58

; Sequence 58, Application US/09004729  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wu Hunter, Shirley  
 ; APPLICANT: Stiegler, Gary  
 ; APPLICANT: Gaines, Patrick J.  
 ; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID  
 ; TITLE OF INVENTION: MOLECULES AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 103  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross P.C.  
 ; STREET: 1700 Lincoln Street, Suite 3500  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/004,729  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/749,699  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Connell, Gary J.  
 ; REGISTRATION NUMBER: 32,020  
 ; REFERENCE/DOCKET NUMBER: 2618-25-C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 58:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 34 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (primer)  
 US-09-004-729-58

Query Match 71.0%; Score 14.2; DB 14; Length 34;  
 Best Local Similarity 84.2%; Pred. No. 8.3e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 gttaggatggtccgctca 20  
 ||||| ||||| ||||| |||||  
 Db 13 GTTAGGATGTCGCCGTC 31

## RESULT 13

US-09-004-755-58  
 ; Sequence 58, Application US/09004755  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wu Hunter, Shirley  
 ; APPLICANT: Stiegler, Gary  
 ; APPLICANT: Gaines, Patrick J.  
 ; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID  
 ; TITLE OF INVENTION: MOLECULES AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 103  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross P.C.  
 ; STREET: 1700 Lincoln Street, Suite 3500  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,755  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/749,699  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-25-C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (primer)  
US-09-004-755-58

Query Match 71.0%; Score 14.2; DB 14; Length 34;  
Best Local Similarity 84.2%; Pred. No. 8.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttaggatggtgccgtca 20  
||||| ||||| ||||| |||||  
Db 13 GTTAGCGATCGTCCGTC 31

RESULT 14  
US-09-171-741C-58  
Sequence 58, Application US/09171741C  
GENERAL INFORMATION:  
APPLICANT: Grieve, Robert B.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wu Hunter, Shirley  
APPLICANT: Frank, Glenn R.  
APPLICANT: Stiegler, Gary  
APPLICANT: Gaines, Patrick J.  
APPLICANT: Silver, Gary  
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 2618-25-C4-PUS  
CURRENT APPLICATION NUMBER: US/09/171,741C  
CURRENT FILING DATE: 1999-04-23  
PRIOR APPLICATION NUMBER: PCT/US97/06121  
PRIOR FILING DATE: 1997-04-04  
NUMBER OF SEQ ID NOS: 165  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 58  
LENGTH: 34  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-171-741C-58

Query Match 71.0%; Score 14.2; DB 15; Length 34;  
Best Local Similarity 84.2%; Pred. No. 8.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttaggatggtgccgtca 20  
||||| ||||| ||||| |||||  
Db 13 gttagcgatcgcccgctca 31

RESULT 15  
US-07-896-094-1/C  
Sequence 1, Application US/07896094  
GENERAL INFORMATION:  
APPLICANT: Sheiness, Diana K.  
APPLICANT: Adams, Trevor H.  
APPLICANT: Stamm, Michael P.  
APPLICANT: Cangelosi, Gerard A.  
TITLE OF INVENTION: Methods and Pharmaceutical Kits Useful  
TITLE OF INVENTION: for Detecting Microorganisms Associated with Vaginal  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/896,094  
FILING DATE: 19920529  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 11652-73-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-07-896-094-1

Query Match 69.0%; Score 13.8; DB 3; Length 24;  
Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ttagggatggtgccgtc 19  
||||| ||||| ||||| |||||  
Db 18 TTTGGGATGGAGCCGTC 2

Search completed: October 2, 2001, 21:50:15  
Job time: 24528 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:14 ; Search time 17695.9 Seconds  
(without alignments)  
16.701 Million cell updates/sec

Title: US-09-757-100B-12

Perfect score: 20  
Sequence: 1 cctgacatcagtagcatctc 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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39: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*  
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44: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*  
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49: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq.\*  
50: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq.\*  
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53: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*  
54: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*  
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57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*  
58: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*  
59: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*  
60: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	100.0	20	1	PCT-US00-18999-12	Sequence 12, Appl
2	20	100.0	20	17	US-09-377-310-12	Sequence 12, Appl
3	20	100.0	20	29	US-09-757-100B-12	Sequence 16, Appl
C 4	16.4	82.0	20	1	PCT-US00-07678-16	Sequence 16, Appl
C 5	16.4	82.0	20	20	US-09-535-008-16	Sequence 16, Appl
C 6	15.8	79.0	25	55	US-60-233-166-196919	Sequence 196919,
C 7	15.8	79.0	25	55	US-60-233-166-296426	Sequence 296426,
8	15	75.0	15	1	PCT-US00-18999-32	Sequence 32, Appl
9	15	75.0	15	17	US-09-377-310-32	Sequence 32, Appl
10	15	75.0	15	29	US-09-757-100B-32	Sequence 32, Appl
C 11	14.8	74.0	20	30	US-09-794-422-41	Sequence 41, Appl
C 12	14.2	71.0	25	55	US-60-233-166-198167	Sequence 198167,
C 13	14.2	71.0	25	55	US-60-233-166-198168	Sequence 198168,
C 14	14.2	71.0	25	55	US-60-233-166-303481	Sequence 303481,
C 15	13.8	69.0	17	8	US-08-435-632-1431	Sequence 1431, Ap
C 16	13.8	69.0	17	11	US-08-777-920-1431	Sequence 1431, Ap
C 17	13.8	69.0	21	25	US-09-657-472-257	Sequence 257, App
C 18	13.8	69.0	25	55	US-60-232-638-119646	Sequence 119646,
C 19	13.8	69.0	25	55	US-60-233-166-6055	Sequence 6055, Ap
C 20	13.8	69.0	25	55	US-60-233-166-226952	Sequence 226952,
C 21	13.8	69.0	25	55	US-60-233-166-290790	Sequence 290790,
C 22	13.6	68.0	25	26	US-09-660-220-81834	Sequence 81834, A
C 23	13.6	68.0	25	55	US-60-234-017-13449	Sequence 13449, A
C 24	13.6	68.0	25	55	US-60-234-017-361774	Sequence 361774,
C 25	13.6	68.0	25	55	US-60-234-049-104369	Sequence 104369,
C 26	13.6	68.0	39	1	PCT-US99-29963-38	Sequence 38, Appl
C 27	13.6	68.0	40	1	PCT-US99-29963-37	Sequence 37, Appl
C 28	13.6	68.0	42	3	US-07-904-068A-64	Sequence 64, Appl
C 29	13.6	68.0	42	5	US-08-161-739-64	Sequence 64, Appl
C 30	13.6	68.0	42	5	US-08-165-699-64	Sequence 64, Appl
C 31	13.6	68.0	42	11	US-08-728-463-36	Sequence 36, Appl
C 32	13.6	68.0	42	11	US-08-728-463-73	Sequence 73, Appl
C 33	13.6	68.0	42	11	US-08-728-463B-36	Sequence 36, Appl
C 34	13.6	68.0	42	11	US-08-728-463B-73	Sequence 73, Appl
C 35	13.6	68.0	42	11	US-08-758-417-36	Sequence 36, Appl
C 36	13.6	68.0	42	11	US-08-758-417-73	Sequence 73, Appl
C 37	13.6	68.0	42	11	US-08-758-417A-36	Sequence 36, Appl
C 38	13.6	68.0	42	11	US-08-758-417A-73	Sequence 73, Appl
C 39	13.4	67.0	25	26	US-09-660-220-138856	Sequence 138856,
C 40	13.4	67.0	25	26	US-09-660-220-138858	Sequence 138858,
C 41	13.4	67.0	25	26	US-09-660-220-138859	Sequence 138859,
C 42	13.4	67.0	25	55	US-60-232-638-14816	Sequence 14816, A
C 43	13.4	67.0	25	55	US-60-233-166-296504	Sequence 296504,
C 44	13.2	66.0	21	17	US-09-357-273A-11	Sequence 11, Appl
C 45	13.2	66.0	25	55	US-60-233-166-147576	Sequence 147576,

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-12  
; Sequence 12, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-12

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 cctgacatcagtagcatctc 20

RESULT 2  
US-09-377-310-12  
; Sequence 12, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-12

Query Match 100.0%; Score 20; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20  
|||||  
DB 1 cctgacatcagtagcatctc 20

RESULT 3  
US-09-757-100B-12  
; Sequence 12, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR FILING DATE: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-12

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Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20  
|||||  
DB 1 cctgacatcagtagcatctc 20

RESULT 4  
PCT-US00-07678-16/c  
; Sequence 16, Application PC/TUS0007678  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Alexander K.C.  
; APPLICANT: Tavtigian, Sean V.  
; APPLICANT: Teng, David H.-F.  
; APPLICANT: Myriad Genetics, Inc.  
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE  
; FILE REFERENCE: 2318-259-PCT  
; CURRENT APPLICATION NUMBER: PCT/US00/07678  
; CURRENT FILING DATE: 2000-03-23  
; EARLIER APPLICATION NUMBER: U.S. 60/125,806  
; EARLIER FILING DATE: 1999-03-23  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US00-07678-16

Query Match 82.0%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 6.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cctgacatcagtagcatctc 19  
|||  
DB 20 CTGGCATCAGTAGCATCT 3

RESULT 5  
US-09-535-008-16/c  
; Sequence 16, Application US/09535008  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Alexander K.C.  
; APPLICANT: Tavtigian, Sean V.  
; APPLICANT: Teng, David H.-F.

; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE  
; FILE OF INVENTION: AND OTHER CANCER TYPES  
; FILE REFERENCE: 2318-259  
; CURRENT APPLICATION NUMBER: US/09/535,008  
; CURRENT FILING DATE: 2000-03-23  
; EARLIER APPLICATION NUMBER: U.S. 60/125,806  
; EARLIER FILING DATE: 1999-03-23  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-535-008-16

Query Match 82.0%; Score 16.4; DB 20; Length 20;  
Best Local Similarity 94.4%; Pred. No. 6.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ctgacatcagtagcatct 19  
||| ||||| ||||| |||||  
Db 20 CTGCATCAGTAGCATCT 3

RESULT 6  
US-60-233-166-196919/c  
; Sequence 196919, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mitmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 196919  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA998576  
US-60-233-166-196919

Query Match 79.0%; Score 15.8; DB 55; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatct 19  
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Db 19 CCTGACACCAAGCATCT 1

RESULT 7  
US-60-233-166-296426/c  
; Sequence 296426, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mitmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 296426  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF639536  
US-60-233-166-296426

Query Match 79.0%; Score 15.8; DB 55; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ctgacatcagtagcatctc 20  
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Db 22 CTGCATAAGTAGCACCTC 4

RESULT 8  
PCT-US00-18999-32  
; Sequence 32, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-32

Query Match 75.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgacatcagtagcat 17  
||||| ||||| ||||| |||||  
Db 1 tgacatcagtagcat 15

RESULT 9  
US-09-377-310-32  
; Sequence 32, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-32

Query Match 75.0%; Score 15; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;



;; TITLE OF INVENTION: Genome  
;; FILE REFERENCE: 3112  
;; CURRENT APPLICATION NUMBER: US/60/233,166  
;; CURRENT FILING DATE: 2000-10-24  
;; NUMBER OF SEQ ID NOS: 420907  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 303481  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Rattus norvegicus  
;; PUBLICATION INFORMATION:  
;; DATABASE ACCESSION NUMBER: GenBank D10757  
US-60-233-166-303481

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 7.9e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 cctgacatcagtagcatct 19  
||||| |||||  
Db 3 cctgaagtgcagtagcatct 21

## RESULT 15

US-08-435-632-1431/c  
; Sequence 1431, Application US/08435632  
; GENERAL INFORMATION:

;; APPLICANT: Stinchcomb, Dan T.  
;; APPLICANT: Draper, Kenneth  
;; APPLICANT: McSwiggen, James  
;; APPLICANT: Jarvis, Thale  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
;; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
;; NUMBER OF SEQUENCES: 2627  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

;; MEDIUM TYPE: storage

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: IBM P.C. DOS 5.0

;; SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/435,632

;; FILING DATE: 05-MAY-1995

;; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/373,124

;; FILING DATE: January 13, 1995

;; APPLICATION NUMBER: 08/245,466

;; FILING DATE: May 18, 1994

;; APPLICATION NUMBER: 08/192,943

;; FILING DATE: February 7, 1994

;; APPLICATION NUMBER: 07/987,132

;; FILING DATE: December 7, 1992

;; APPLICATION NUMBER: 07/936,422

;; FILING DATE: August 26, 1992

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Warburg, Richard

;; REGISTRATION NUMBER: 32,327

;; REFERENCE/DOCKET NUMBER: 209/035

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (213) 489-1600

;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510

## ; INFORMATION FOR SEQ ID NO: 1431:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-435-632-1431

Query Match 69.0%; Score 13.8; DB 8; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 gacatcagtagcatctc 20  
||||| |||||  
Db 17 GACATCAGGAGCACTC 1

Search completed: October 2, 2001, 21:50:15  
Job time: 24528 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 12:00:36 ; Search time 417.38 Seconds  
(without alignments)  
9.071 Million cell updates/sec

Title: US-09-757-100B-3

Perfect score: 20

Sequence: 1 ccgcgggctcacagtgtcg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

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4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-3
2	15	75.0	15	3	US-09-377-310-23
3	13.8	69.0	31	3	US-09-282-996-18
4	13.2	66.0	33	1	US-08-361-337-41
5	12.2	61.0	18	3	US-09-344-579-40
6	12.2	61.0	31	2	US-08-732-612-6
7	12.2	61.0	39	2	US-08-732-612-11
8	12.2	61.0	40	3	US-09-135-639-8
9	12.2	61.0	40	3	US-09-135-639-10
10	12.2	61.0	50	4	US-09-315-886C-5
11	12	60.0	41	3	US-08-751-359-9
12	11.8	59.0	16	1	US-08-640-378-13
13	11.8	59.0	22	1	US-08-242-403A-38
14	11.8	59.0	22	1	US-08-774-128-38
15	11.8	59.0	22	5	PCT-US95-05602-38
16	11.8	59.0	22	5	PCT-US95-05816-38
17	11.8	59.0	29	1	US-08-640-378-3
18	11.8	59.0	30	1	US-08-640-378-4
19	11.8	59.0	30	1	US-08-640-378-5
20	11.8	59.0	35	1	US-08-289-953-1
21	11.8	59.0	35	5	PCT-US95-09195-1
22	11.8	59.0	36	1	US-07-744-282C-19
23	11.8	59.0	36	5	PCT-US92-06821A-19
24	11.8	59.0	44	1	US-08-242-403A-34
25	11.8	59.0	44	1	US-08-774-128-34
26	11.8	59.0	44	5	PCT-US95-05602-34
27	11.8	59.0	44	5	PCT-US95-05816-34

28 11.6 58.0 24 1 US-08-139-540-8  
29 11.6 58.0 24 1 US-08-634-826-8  
30 11.6 58.0 24 3 US-09-115-175-8  
31 11.6 58.0 25 1 US-08-096-947-6  
32 11.6 58.0 25 1 US-08-096-947-7  
33 11.6 58.0 25 1 US-08-096-947-9  
34 11.6 58.0 25 1 US-07-919-140B-6  
35 11.6 58.0 25 1 US-07-919-140B-7  
36 11.6 58.0 25 1 US-07-919-140B-9  
37 11.6 58.0 25 2 US-08-924-763-7  
38 11.6 58.0 25 3 US-08-617-256-12  
39 11.6 58.0 25 4 US-09-287-141-12  
40 11.6 58.0 25 4 US-09-431-613-12  
41 11.6 58.0 25 4 US-09-504-245-12  
42 11.6 58.0 25 4 US-09-287-682-12  
43 11.6 58.0 25 4 US-09-358-972-246  
44 11.6 58.0 25 4 US-09-397-766-12  
45 11.6 58.0 25 5 PCT-US93-06939-9

#### ALIGNMENTS

RESULT 1  
US-09-377-310-3  
; Sequence 3, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-3

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgcgggctcacagtgtcg 20  
Db 1 ccgcgggctcacagtgtcg 20

RESULT 2  
US-09-377-310-23  
; Sequence 23, Application US/09377310B  
; Patent No. 6133031  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-23

Query Match      75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gcggggtcacagtgg 17
    |||||
DB 1 gcggggtcacagtgg 15

RESULT 3
US-09-282-996-18/c
; Sequence 18, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282.996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 18
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer fsA22
US-09-282-996-18

Query Match      69.0%; Score 13.8; DB 3; Length 31;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggtcacagtgg 17
    |||||
DB 25 CACGGGATCACAGTGG 9

RESULT 4
US-08-361-337-41
; Sequence 41, Application US/08361337
; Patent No. 5728519
; GENERAL INFORMATION:
; APPLICANT: Levenbook, Inessa S.
; APPLICANT: Chumakov, Konstantin M.
; APPLICANT: No. 5728519wood, Laurie P.
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
; TITLE OF INVENTION: ATTENUATED LIVE VACCINES
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/361.337
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.634
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-361-337-41

Query Match      66.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ccgcgggtcacagtgg 18
    |||||
DB 9 CCGGGGTTCAAAGTAGT 26

RESULT 5
US-09-344-579-40
; Sequence 40, Application US/09344579
; Patent No. 6054316
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
; FILE REFERENCE: RTS-0063
; CURRENT APPLICATION NUMBER: US/09/344.579
; CURRENT FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-579-40

Query Match      61.0%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gcggggtcacagtggtc 19
    |||||
DB 2 gccgggtcagggtggtc 18

RESULT 6
US-08-732-612-6
; Sequence 6, Application US/08732612
; Patent No. 5922583
; GENERAL INFORMATION:
; APPLICANT: MORSEY, MOHAMAD A.
; TITLE OF INVENTION: METHODS FOR PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: PLASMIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVE., NW
; CITY: WASHINGTON
; STATE: DC
```



; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Anabaena variabilis  
US-09-135-639-10

Query Match 61.0%; Score 12.2; DB 3; Length 40;  
Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccgcgggtcacagtgg 17  
||| ||||| |||  
Db 8 ccccggtctcaagtgg 24

RESULT 10  
US-09-315-886C-5  
; Sequence 5, Application US/09315886C  
; Patent No. 6225063  
; GENERAL INFORMATION:  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Yarus, Michael  
; TITLE OF INVENTION: RNA Channels in Biological Membranes  
; FILE REFERENCE: UTC-03444  
; CURRENT APPLICATION NUMBER: US/09/315,886C  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 60/086,492  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 50  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
US-09-315-886C-5

Query Match 61.0%; Score 12.2; DB 4; Length 50;  
Best Local Similarity 64.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 gcggggtcacagtgtc 19  
||| :|||:| :|  
Db 23 gggggguucacagugauc 39

RESULT 11  
US-08-751-359-9/C  
; Sequence 9, Application US/08751359  
; Patent No. 6143559  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/751,359  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 510  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-751-359-9

Query Match 60.0%; Score 12; DB 3; Length 41;  
Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ccgcgggtcacagtgtcg 20  
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Db 24 CCCCCTGCCACAGTCATCG 5

RESULT 12  
US-08-640-378-13/c  
; Sequence 13, Application US/08640378  
; Patent No. 5811269  
; GENERAL INFORMATION:  
; APPLICANT: Nadeau, James G.  
; APPLICANT: Dean, Cheryl H.  
; APPLICANT: Schram, James L.  
; APPLICANT: Howard, Deborah R.  
; APPLICANT: Dey, Margaret S.  
; APPLICANT: Wright, David J.  
; TITLE OF INVENTION: DETECTION OF MYCOBACTERIA BY MULTIPLEX  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and  
; ADDRESSEE: Company  
; STREET: 1 Becton Drive  
; CITY: Franklin Lakes  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07417  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/640,378  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fugit, Donna R.  
; REGISTRATION NUMBER: 32,135  
; REFERENCE/DOCKET NUMBER: P-3625  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-640-378-13

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Query Match          59.0%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggctcacagt 15
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Db 15 CCGCATGCTCACAGT 1

RESULT 13
US-08-242-403A-38
; Sequence 38, Application US/08242403A
; Patent No. 5631130
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
; APPLICANT: Sample-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,403A
; FILING DATE: May 13, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5370.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-4884
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
; US-08-242-403A-38

Query Match          59.0%; Score 11.8; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggctcacagt 15
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Db 7 CCGCAGCTCACAGT 21

RESULT 14
US-08-774-128-38
; Sequence 38, Application US/08774128
; Patent No. 5786149
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
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```
; APPLICANT: Sample-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,128
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/242,403
; FILING DATE: May 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5370.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-4884
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
; US-08-774-128-38

Query Match          59.0%; Score 11.8; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggctcacagt 15
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Db 7 CCGCAGCTCACAGT 21

RESULT 15
PCT-US95-05602-38
; Sequence 38, Application PC/TUS9505602
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis A.H.
; APPLICANT: Sample-Facey, I.E.
; APPLICANT: Manlove, M.T.
; APPLICANT: Solomon, N.A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;;  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC\_DOS/MS\_DOS  
;; SOFTWARE: Wordperfect  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/05602  
;; FILING DATE: May 13, 1994  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Thomas D. Brainard  
;; REGISTRATION NUMBER: 32,459  
;; REFERENCE/DOCKET NUMBER: 5370.PC.01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 708/937-4884  
;; TELEFAX: 708/938-2623  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: Synthetic DNA  
PCT-US95-05602-38

Query Match 59.0%; Score 11.8; DB 5; Length 22;  
Best Local Similarity 86.7%; Pred. No. 1.8e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 7 CCGCACGCTCACAGT 21

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Job time: 14588 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-757-100B-11

Perfect score: 20

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Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6	15.2	76.0	25	55	US-60-233-166-329526
7	15.2	76.0	25	55	US-60-233-166-329643
8	15.2	76.0	25	55	US-60-233-166-329644
9	15	75.0	15	1	PCT-US00-18999-31
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11	15	75.0	15	29	US-09-757-100B-31
12	14.8	74.0	25	55	US-60-234-017-22548
13	14.4	72.0	25	55	US-60-233-620-18028
14	14.2	71.0	25	55	US-60-234-017-142091
15	14.2	71.0	25	55	US-60-234-017-142072
16	14.2	71.0	25	55	US-60-234-017-439150
17	13.8	69.0	25	55	US-60-233-166-188071
18	13.8	69.0	25	55	US-60-233-166-329525
19	13.8	69.0	25	55	US-60-233-166-329641
20	13.8	69.0	25	55	US-60-234-017-22543
21	13.8	69.0	25	55	US-60-234-017-365211
22	13.6	68.0	25	26	US-09-660-220-54619
23	13.6	68.0	25	55	US-60-233-166-51615
24	13.6	68.0	25	55	US-60-233-166-409875
25	13.6	68.0	25	55	US-60-234-017-24188
26	13.6	68.0	25	55	US-60-234-017-42888
27	13.6	68.0	25	55	US-60-234-017-57516
28	13.6	68.0	25	55	US-60-234-017-153880
29	13.6	68.0	25	55	US-60-234-017-523545
30	13.4	67.0	21	3	US-07-918-259-7
31	13.4	67.0	25	26	US-09-660-220-71111
32	13.4	67.0	25	55	US-60-233-166-63810
33	13.4	67.0	25	55	US-60-233-166-63910
34	13.2	66.0	25	26	US-09-660-220-111255
35	13.2	66.0	25	26	US-09-660-220-111262
36	13.2	66.0	25	26	US-09-660-220-111262
37	13.2	66.0	25	55	US-60-232-638-101075
38	13.2	66.0	25	55	US-60-233-166-95260
39	13.2	66.0	25	55	US-60-233-166-201189
40	13.2	66.0	25	55	US-60-233-166-320476
41	13.2	66.0	25	55	US-60-233-166-335443
42	13.2	66.0	25	55	US-60-233-166-397247
43	13.2	66.0	25	55	US-60-233-620-125356
44	13.2	66.0	25	55	US-60-234-017-174077
45	13.2	66.0	25	55	US-60-234-017-215290

## ALIGNMENTS

RESULT 1  
PCT-US00-18999-11  
; Sequence 11, Application PC/TU0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-11

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtaccagggtgagctcttag 20  
|||||

Db 1 agtaccagggtgagctcttag 20

RESULT 2  
US-09-377-310-11  
; Sequence 11, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-11

Query Match 100.0%; Score 20; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtaccagggtgagctcttag 20  
|||||

Db 1 agtaccagggtgagctcttag 20

RESULT 3  
US-09-757-100B-11  
; Sequence 11, Application US/09757100B

; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-11

Query Match 100.0%; Score 20; DB 29; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtaccagggtgagctcttag 20  
|||||

Db 1 agtaccagggtgagctcttag 20

RESULT 4  
US-60-233-166-320910/c  
; Sequence 320910, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 320910  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank L08493  
US-60-233-166-320910

Query Match 79.0%; Score 15.8; DB 55; Length 25;  
Best Local Similarity 89.5%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gtaccagggtgagctcttag 20  
|||

Db 24 GTATTCAGGTGAGCTCTTAG 6

RESULT 5  
US-60-233-357-9034/c  
; Sequence 9034, Application US/602333357  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3114



; CURRENT APPLICATION NUMBER: US/60/233,357  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 21305  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9034  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank L08493  
US-60-233-357-9034

Query Match 79.0%; Score 15.8; DB 55; Length 25;  
Best Local Similarity 89.5%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gtaccaccaggtagtcttag 20  
||| ||||||| |||||

Db 24 GTAATCAGGTGAGTCTTAG 6

## RESULT 6

US-60-233-166-329526  
; Sequence 329526, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 329526  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank M31725  
US-60-233-166-329526

Query Match 76.0%; Score 15.2; DB 55; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccaccaggtagtcttag 20  
||| ||||||| |||||

Db 3 agaaccaccaggtaaatcttag 22

## RESULT 7

US-60-233-166-329643  
; Sequence 329643, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 329643  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank M31725  
US-60-233-166-329643

Query Match 76.0%; Score 15.2; DB 55; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccaccaggtagtcttag 20  
||| ||||||| |||||

Db 6 agaaccaccaggtaaatcttag 25

## RESULT 8

US-60-233-166-329644  
; Sequence 329644, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 329644  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank M31725  
US-60-233-166-329644

Query Match 76.0%; Score 15.2; DB 55; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccaccaggtagtcttag 20  
||| ||||||| |||||

Db 5 agaaccaccaggtaaatcttag 24

## RESULT 9

PCT-US00-18999-31  
; Sequence 31, Application PC/TUS0018999  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0476  
; CURRENT APPLICATION NUMBER: PCT/US00/18999  
; CURRENT FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
PCT-US00-18999-31

Query Match 75.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 taccaccaggtagtct 17

Db 1 taccaggtagtct 15  
|||||

## RESULT 10

US-09-377-310-31  
; Sequence 31, Application US/09377310A  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0389  
; CURRENT APPLICATION NUMBER: US/09/377,310A  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-310-31

Query Match 75.0%; Score 15; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccaggtagtct 17  
|||||

## RESULT 11

US-09-757-100B-31  
; Sequence 31, Application US/09757100B  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Gaarde, William A.  
; APPLICANT: Nero, Pamela S.  
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
; FILE REFERENCE: ISPH-0533  
; CURRENT APPLICATION NUMBER: US/09/757,100B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/377,310  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/US00/18999  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-757-100B-31

Query Match 75.0%; Score 15; DB 29; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccaggtagtct 17  
|||||

## RESULT 12

US-60-234-017-22548

; Sequence 22548, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22548  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AJ001261  
US-60-234-017-22548

Query Match 74.0%; Score 14.8; DB 55; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gtaccaggtagtctta 19  
|||||

Db 5 gtaaccatgtgagtctta 22  
|||||

## RESULT 13

US-60-233-620-18028  
; Sequence 18028, Application US/60233620  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of  
; FILE REFERENCE: 3116  
; CURRENT APPLICATION NUMBER: US/60/233,620  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 131820  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18028  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AC005724  
US-60-233-620-18028

Query Match 72.0%; Score 14.4; DB 55; Length 25;  
Best Local Similarity 93.8%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 cccaggtagtcttag 20  
|||||

Db 10 cccagctgagtcttag 25  
|||||

## RESULT 14

US-60-234-017-142091  
; Sequence 142091, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 142091  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF591702  
; US-60-234-017-142091

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 gtaccacaggtagtcttag 20  
||| ||||| ||||| ||  
Db 4 gtaccacaggtaagtctgag 22

RESULT 15  
US-60-234-017-420702  
; Sequence 420702, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, M  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 420702  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AU024707  
; US-60-234-017-420702

Query Match 71.0%; Score 14.2; DB 55; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 agtaccacaggtagtcttta 19  
||| ||||| ||||| ||  
Db 1 agtccccaagtgtagcttta 19

Search completed: October 2, 2001, 21:50:14  
Job time: 24527 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:02 ; Search time 2173.58 Seconds  
(without alignments)  
19.290 Million cell updates/sec

Title: US-09-757-100B-11

Perfect score: 20

Sequence: 1 agtaccaggtagcttag 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	12.8	64.0	25	6	US-09-857-581-65
2	12.4	62.0	33	7	US-09-672-217-122
3	12.4	62.0	33	7	US-09-672-217-223
4	12	60.0	22	1	PCT-US00-00358-16
5	12	60.0	25	6	US-09-866-108-4143
6	12	60.0	25	6	US-09-866-108-4144
7	12	60.0	25	6	US-09-866-108-4145
8	12	60.0	25	6	US-09-866-108-4146
9	12	60.0	25	6	US-09-866-108-4147
10	12	60.0	25	6	US-09-866-108-4148
11	12	60.0	44	8	US-60-252-833-24181
12	11.8	59.0	17	6	US-09-546-745A-4802
13	11.6	58.0	29	7	US-09-724-671-10607
14	11.6	58.0	48	8	US-60-253-457-42408
15	11.4	57.0	26	6	US-09-863-806-69
16	11.4	57.0	31	6	US-09-801-274-1705
17	11.2	56.0	17	6	US-09-522-240A-30
18	11.2	56.0	17	6	US-09-866-108-7712
19	11.2	56.0	17	6	US-09-866-108-7713
20	11.2	56.0	17	6	US-09-513-063-18
21	11.2	56.0	17	6	US-09-817-879-2232
22	11.2	56.0	17	6	US-09-817-879-2233
23	11.2	56.0	20	6	US-09-895-007-115
24	11.2	56.0	20	7	US-09-920-313-115
25	11.2	56.0	20	7	US-09-659-845A-82

c	26	11.2	56.0	20	7	US-09-899-440-1	Sequence 1, Appl
	27	11.2	56.0	22	7	US-09-648-103B-51	Sequence 51, Appl
	28	11.2	56.0	25	6	US-09-866-108-12604	Sequence 12604, A
	29	11.2	56.0	25	6	US-09-866-108-12605	Sequence 12605, A
	30	11.2	56.0	25	6	US-09-866-108-12606	Sequence 12606, A
	31	11.2	56.0	25	6	US-09-866-108-12607	Sequence 12607, A
	32	11.2	56.0	25	6	US-09-866-108-12608	Sequence 12608, A
	33	11.2	56.0	25	6	US-09-866-108-12609	Sequence 12609, A
	34	11.2	56.0	25	6	US-09-866-108-12610	Sequence 12610, A
	35	11.2	56.0	25	6	US-09-866-108-12611	Sequence 12611, A
	36	11.2	56.0	25	6	US-09-866-108-12612	Sequence 12612, A
	37	11.2	56.0	25	6	US-09-866-108-12613	Sequence 12613, A
	38	11.2	56.0	25	7	US-09-648-103B-49	Sequence 49, Appl
	39	11.2	56.0	36	5	US-09-274-553C-2830	Sequence 2830, Ap
	40	11.2	56.0	38	7	US-09-864-785-1301	Sequence 1301, Ap
	41	11.2	56.0	50	5	US-09-899-011A-308	Sequence 308, App
	42	11	55.0	25	5	US-09-930-803-7	Sequence 7, Appl
	43	11	55.0	25	6	US-09-866-108-4142	Sequence 4142, Ap
	44	11	55.0	25	6	US-09-866-108-4149	Sequence 4149, Ap
	45	11	55.0	25	6	US-09-866-108-4254	Sequence 4254, Ap

ALIGNMENTS

RESULT 1  
US-09-857-581-65/c  
; Sequence 65, Application US/09857581  
; GENERAL INFORMATION:  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase  
; FILE REFERENCE: BB1339 PCT  
; CURRENT APPLICATION NUMBER: US/09/857,581  
; CURRENT FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 60/117,769  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: 60/144,783  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/156,094  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 65  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR PRIMER  
US-09-857-581-65

Query Match 64.0%; Score 12.8; DB 6; Length 25;  
Best Local Similarity 87.3%; Pred. No. 2.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cccaggtagcttag 20  
|||||  
Db 17 CCCAGGTGAGTTTCAG 2

RESULT 2  
US-09-672-217-122  
; Sequence 122, Application US/09672217  
; GENERAL INFORMATION:  
; APPLICANT: DIAZ, JAKA  
; APPLICANT: FELL, JACK  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI  
; FILE REFERENCE: 086222/0143  
; CURRENT APPLICATION NUMBER: US/09/672,217  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/156,598  
; PRIOR FILING DATE: 1999-09-29

```
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-122

Query Match      62.0%; Score 12.4; DB 7; Length 33;
Best Local Similarity 92.9%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 acccaggtgagtct 17
   |||||
Db 17 acccaggtgagtat 30

RESULT 3
; Sequence 223, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143
; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 223
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-223

Query Match      62.0%; Score 12.4; DB 7; Length 33;
Best Local Similarity 92.9%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 acccaggtgagtct 17
   |||||
Db 17 acccaggtgagtat 30

RESULT 4
; Sequence 16, Application PC/TUS0000358
; GENERAL INFORMATION:
; APPLICANT: pecker, iris
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY DISTANTLY HOMOLOG
; FILE REFERENCE: 00/20105
; CURRENT APPLICATION NUMBER: PC/TUS00/00358
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/140,801
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Synthetic Oligonucleotide
PC-TUS00-00358-16
```

```
Query Match      60.0%; Score 12; DB 1; Length 22;
Best Local Similarity 75.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccacaggtgagtccttag 20
   ||| |||||
Db 2 agcagccaggtgagcccaag 21

RESULT 5
; Sequence 4143, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4143
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4143
```

```
Query Match      60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccacaggtgagtccttag 20
   ||| |||||
Db 6 agaagacaggtgagcctcag 25
```

## RESULT 6

US-09-866-108-4144  
; Sequence 4144, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aemica Sequence Listing Engine  
; SEQ ID NO 4144  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4144

Query Match 60.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 75.0%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 agtaccagggtgagcttag 20  
||| ||||| |||||  
Db 5 agaagacaggtgagcctcag 24

## RESULT 7

US-09-866-108-4145  
; Sequence 4145, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aemica Sequence Listing Engine  
; SEQ ID NO 4145  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4145

Query Match 60.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 75.0%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 agtaccagggtgagcttag 20  
||| ||||| |||||  
Db 4 agaagacaggtgagcctcag 23

## RESULT 8

US-09-866-108-4146  
; Sequence 4146, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 4146  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4146

Query Match 60.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 75.0%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctcttag 20  
||| | ||||| |||  
Db 3 agaagacagggtgagcctcag 22

RESULT 9  
US-09-866-108-4147  
; Sequence 4147, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 4147  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4147

Query Match 60.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 75.0%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctcttag 20  
||| | ||||| |||  
Db 2 agaagacagggtgagcctcag 21

RESULT 10  
US-09-866-108-4148  
; Sequence 4148, Application US/09866108  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670



; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 4148  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4148

Query Match 60.0%; Score 12; DB 6; Length 25;  
Best Local Similarity 75.0%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctcttag 20  
||| ||||| ||| |||  
Db 1 agaagacagggtgagcctcag 20

RESULT 11  
US-60-252-833-24181/c  
; Sequence 24181, Application US/60252833  
; GENERAL INFORMATION:  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions isolated from bovine  
; TITLE OF INVENTION: tissues and methods for their use.  
; FILE REFERENCE: 1052P2  
; CURRENT APPLICATION NUMBER: US/60/252,833  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 43535  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24181  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Bovine  
US-60-252-833-24181

Query Match 60.0%; Score 12; DB 8; Length 44;  
Best Local Similarity 75.0%; Pred. No. 6.4e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctcttag 20  
||||| |||| || ||||  
Db 21 AGTACTCAGGAGGAGCTTTAG 2

RESULT 12  
US-09-546-745A-4802/c  
; Sequence 4802, Application US/09546745A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: Zwick, Michael  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules  
; FILE REFERENCE: 237/193  
; CURRENT APPLICATION NUMBER: US/09/546,745A  
; CURRENT FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 7043  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4802  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-546-745A-4802

Query Match 59.0%; Score 11.8; DB 6; Length 17;  
Best Local Similarity 86.7%; Pred. No. 7.1e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ccagggtgagctcttag 20  
||||| ||||| |||  
Db 15 CCAGGTGAGGCGTAG 1

RESULT 13  
US-09-724-671-10607/c  
; Sequence 10607, Application US/09724671  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 1050U2  
; CURRENT APPLICATION NUMBER: US/09/724,671  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10607  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Mouse  
US-09-724-671-10607

Query Match 58.0%; Score 11.6; DB 7; Length 29;  
Best Local Similarity 77.8%; Pred. No. 1e+04;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctctt 18  
||| ||||| ||| |||  
Db 22 AGTGCCAGGTCAGTGTT 5

RESULT 14  
US-60-253-457-42408  
; Sequence 42408, Application US/60253457  
; GENERAL INFORMATION:  
; APPLICANT: Havukkala, Ilkka J  
; TITLE OF INVENTION: Polynucleotides, isolated from plants  
; TITLE OF INVENTION: and methods for their use.  
; FILE REFERENCE: 1054P2  
; CURRENT APPLICATION NUMBER: US/60/253,457  
; CURRENT FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 48893  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42408  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-60-253-457-42408

Query Match 58.0%; Score 11.6; DB 8; Length 48;  
Best Local Similarity 77.8%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 taccagggtgagctcttag 20  
||| ||||| ||| |||  
Db 9 tacgagggtgagatttcg 26

RESULT 15  
US-09-863-806-69/c

```

; Sequence 69, Application US/09863806
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
; NUMBER OF SEQUENCES: 195
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,806
; FILING DATE: 22-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/038,637
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/152,313
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/146001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-863-806-69

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Query Match      57.0%; Score 11.4; DB 6; Length 26;
Best Local Similarity 92.3%; Pred. NO. 1.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 caggtagatctta 19
        ||| |||||
DB      23 CAAGTGAGTCTTA 11

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Search completed: October 2, 2001, 16:55:02  
Job time: 17665 sec

09/757,100